#007 /C./7.60 CT שבים

18-10-008-989a-7.rad

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OM protein - protein search, using sw model

; Search time 97.3985 Seconds (without alignments) 2272.479 Million cell updates/sec October 18, 2004, 13:22:25

Run on:

US-10-658-989A-2 3488 1 GPPGEPGPTGLPGPPGERGG.....GEQGVPGDLGAPGPSGPAGG

617

Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	991 Human rec	17 Adq26217	92 Adm48392 Human		03	0 Aay84540	38 Aay8453	485 Aaw68485 Human rec	Add4505	55	051 Add45051 Human Pro	535 Aae02535 Porcine	50 Ade87050	47 Abg93947 Human	6 Human	1 Ade87051	1 Aay84541 Amino	39 Aay84539	1 Aar71701	122 Aay96122 Collagen	175	73	2	175 Adf13075 Human co	
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Plasma substitute; Gelatin-like protein; plasma expander; human. Human recombinant gelatin-like polypeptide Hu-3. ADM48391 standard; protein; 617 AA. (first entry) Homo sapiens. 03-JUN-2004 ADM48391; RESULT 1 ADM48391

11-SEP-2002; 2002EP-00078745. EP1398324-A1. 17-MAR-2004.

11-SEP-2002; 2002EP-00078745. (FUJF) FUJI PHOTO FILM BV.

Toda Y;

Bouwstra JB,

Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function. WPI; 2004-229415/22.

Example 1; SEQ ID NO 2; 31pp; English.

The present sequence is the protein sequence of recombinant gelatin-like protein Hu-3. This is a trimer of human recombinant gelatin-like protein Hu-1 hDM48390. A claimed composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid osmotic function. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 kDa and at most 50 kDa and an isoelectric point of less than 8. It is especially Hu-1 or Hu-deam ADM48393. The recombinant gelatin-like protein, or a dimer, trimer or tetramer of the protein, is useful as a plasma expander that has a lower clearance rate protein, is useful as a plasma expander that has a lower clearance rate clearance rate and which is less susceptible to proteolytic degradation than presently used gelatin derivatives. Recombinant gelatin-like proteins that are in essence free of hydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically

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active compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the interstitium. Clearance by liver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood
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                                                                                                                      Score 3488; DB 8;
Pred. No. 1.7e-207;
; Mismatches 0;
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The present sequence is the protein sequence of human recombinant gelatin-like polypeptide Hu-3, which has a molecular weight of approximately 54 kba and which contains multiple Gly-Xaa-Yaa triplets. In an example from the invention, recombinant Hu-3 was immobilised on polystyrene beads using a heterobifunctional crosslinking agent, and used in a spinner flask cell culture. A claimed process for the preparation of a cell culture support comprises the step of coating a microcarrier bead with gelatine or gelatine-like protein having a molecular weight of about 40-gelatine or gelatine-like protein having the step of immobilising the gelatine or gelatine-like protein on the microcarrier. In this process, more than 75%, preferably more than 85% and more preferably more than 85% and more preferably more than 85% and more preferably more than 95% of the gelatine or gelatine-like protein has the same molecular weight. The gelatine or gelatine-like protein has the same molecular weight.

The gelatine or gelatine-like protein is recombinately produced to obtain a material of uniform molecular weight and to reduce the risk of contamination with priorectate wegget and to feduce the fish of microbeads of 50-500 um size coated with a gelatine-like protein consisting of at least 95k Gly-Asa-Yaa triplets and containing at least 15k Gly-Asa-Yaa triplets and containing at least 15k foll-line residues and less than 5k of hydroxyproline residues, with a molecular weight distribution showing a maximum between 40 and 200 kba, at least 75k of the protein molecules having a molecular weight within 2k of the maximum. Large-scale production of expressed products can be accomplished with gelatine-coated microcarriers. Preparing cell culture support useful for culturing anchorage dependent cells, involves coating microcarrier bead with gelatine or gelatine-like protein having specific molecular weight. English ∺

Gaps .; 0 Length 617; Indels 100.0%; Score 3488; DB 8; 100.0%; Pred. No. 1.7e-207; ive 0; Mismatches 0;

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300 120 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFPGGLPGPA 180 180 GPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK 240 GPPGERACKPGEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK 240 241 GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP 300 9 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP

The present sequence is the protein sequence of recombinant gelatin-like protein Hu-1 ADM48390. A claimed composition suitable as a substitute for protein Hu-1 ADM48390. A claimed composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid composition. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 kpa and at most 50 kba and an cost 50 kba and an coupled cost 50 kbarmace rate from blood samples containing 19 cost 50 kbarmace rate from the circulation containing 19 cost 50 kbarmaceutically active compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the circulating a more constant plasma level of the medicament. Suitable 480 480 540 540 900 saline 420 GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARQQAGVMGFPGPKGAAGEPGKAGERGVP GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ GPPGAVGPAGKDGEAGAQGPPGPAGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ GPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLP GPAGERGEOGPAGSPGFOGLPGPAGPPGBAGKPGEOGVPGDLGAPGPSGPAGEPGPTGLP GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGPPGPKGAAGEPGKAGERGVP GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT Composition useful as substitute for plasma, comprises solution of st and recombinant gelatin-like protein having colloid osmotic function. Plasma substitute; Gelatin-like protein; plasma expander; human. Human recombinant gelatin-like polypeptide Hu-4. Example 1; SEQ ID NO 3; 31pp; English, Æ ADM48392 standard; protein; 821 GVPGDLGAPGPSGPAGG 617 11-SEP-2002; 2002EP-00078745 11-SEP-2002; 2002EP-00078745 GVPGDLGAPGPSGPAGG ΒV (FUJF) FUJI PHOTO FILM Toda Y; WPI; 2004-229415/22. EP1398324-A1. Bouwstra JB, Homo sapiens 17-MAR-2004. 03-JUN-2004 421 (541 (361 361 481 601 ADM48392; 421 481 601 RESULT 3 ADM48392 원 8 g ò ઠે 임 8 ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
                                                                                                                                                  GPPGEPGPTGL PGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                                                           GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
                                                                                                                        Gaps
medicaments include those involved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as
                                                                                                                        ö
                                                                                           Length 821;
                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen 1 (alpha1) protein helical region.
                                                                                            99.8%; Score 3482; DB 8; L
100.0%; Pred. No. 4.9e-207;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY84544 standard; protein; 1057 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPGDLGAPGPSGPAG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 GVPGDLGAPGPSGPAG 616
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                                                                                            Query Match
Best Local Similarity 100.
Matches 616; Conservative
                                                                     Sequence 821 AA;
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957 GPPGPPGSPGENGPSGPSGPPGSPGSPGKDGLNGLNGLPGPIGPPGPRGRTGDAGPV 1016
                                                                                                                                                                                                                                         GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPPP 510
                                                                                                                                                                                                                                                                       GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 956
                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
557 GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human type 1 (alpha1) collagen protein. 
Peptides derived from the protien were used to demonstrate incorporation of 3,4-dehydro-1-prolline into the peptide, using the method of the invention. The specification describes a method for the incorporation of non-natural amino acid into a polypeptide. The method comprises reacting at least one 3,4-dehydroprolline residue in the polypeptide with an epoxidation reagent from a polypeptide containing at least one 3,4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Incorporating non-natural amino acid into polypeptide, useful e.g. for production of bioadhesives, by epoxidation or substitution of
                                                                                           717 GAAGRVGPPGPSGNAGPPGPPGPPGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                                       Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bloadhesive.
                                                ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                           394 GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                                                                      GARGQAGVMGFPGFKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of human type 1 (alpha1) collagen polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY84403 standard; protein; 1058 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1017 GPPGPPGPPGPPG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US SURGICAL CORP. PAOLELLA D N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dehydroproline residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRUSKIN E A.
BUECHTER D D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-271051/23.
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(BUEC/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3. hydroxyproline and is also useful and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional compensation of salso useful in scudying the structure and function of proteins contended is also useful in scudying the structure and function of proteins enguence represents human collagen (alphal) halical region, which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGPPGARGQA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP---- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGPPGERGVQGPPGPRGFR 536
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                                                                                                                                                                                                                                                                                                                                 Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGPP
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                                                                                                                                                                                                                  Connolly K;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Fig 39A-E; 260pp; English.
                                                                                                                                                                                                                  Zhang G,
                                                                      99EP-00119184.
                                                                                                                    98US-00169768,
                                                                                                                                                                                                               Buechter DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 441; Conservative
                                                                                                                                                                  (USSU ) US SURGICAL CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1057 AA;
                                                                                                                                                                                                                                                                                         N-PSDB; AAA12503
                                                                      07-OCT-1999;
                                                                                                                    09-OCT-1998;
                                                                                                                                                                                                          Gruskin EA,
                      12-APR-2000
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Best Local S
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epoxyproline residue. The method is used for studying the effects of non-
natural amino acids on structure and function of polypeptides. The method
is also useful for commercial production of collagen or mussel adhesive
proteins (which are useful as bioadhesives), and for incorporating a wide
variety of groups, including therapeutic ligands and biological probes,
into polypeptides
        888888888
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Sequence 1058 AA;

12; 558 357 108 417 168 477 597 300 657 341 393 777 453 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 897 GPPGP------AGPACERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603 48 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGKTGPPGKTGPPGPAGQDGRPGPPGARGQA 358 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPPR -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 598 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA--------VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 64.1%; Score 2237.5; DB 3; Length 1058; 60.2%; Pred. No. 3e-130; ive 23; Mismatches 152; Indels 117; Best Local Similarity 60.2 Matches 441; Conservative GDLGAPGPSGPAG GPPGPPGPPGPPG 1018 658 718 778 454 838 511 49 109 169 478 538 301 342 394 213 259 Query Match g à рp δ g ઠે q ઠે a ò g ò g 셤 g gg g ò g ò à ò δ à ठ

셤 ò 셤 ∂ RESULT 6
AAY84540
ID AAX84540 standard; protein; 1107 AA.
XX
AC AAY84540;
XX
DT 25-JUL-2000 (first entry)

Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; decorin; chimera. sequence of a chimeric collagen 1 (alpha1)/decorin protein 굯 Connolly Key Misc-difference 858 /note= "Gly encoded by GCT" ΰ Location/Qualifiers Zhang 99EP-00119184 EA, Buechter DD, (USSU) US SURGICAL CORP WPI; 2000-259138/23. N-PSDB; AAA12500. Homo sapiens. Unidentified. 07-OCT-1999; 09-OCT-1998; 12-APR-2000. EP992586-A2 acid Chimeric. Gruskin Amino Ношо

The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily characylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell for naturally occurring acodons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and conteating the nucleic acid sequence into the cell; and conteating the nucleic acid sequence into the cell; and conteating the nucleic acid sequence into the cell; and conteating the nucleic acid sequence into the cell; and conteating the nucleic acid sequence into the cell; and conteating the nucleic acid sequence of the anino acids to be assimilated hydroxyproline and incorporated into the extracellular matrix protein. The certombinant production of proteins. This is especially useful in the fibronomic production of proteins such as collagen, fibrinogen and fibronomic production of proteins such as collagen, fibrinogen and corporated on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of proteins expensent sequence represents a chimaria collagen (alphan)/decorin corporate in which may be produced using the method of the invention o ព Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful medical implants. Claim 24; Fig 18; 260pp; English

Sequence 1107 AA;

356 416 GPKGSPGEAGRPGEAGLFGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA Query Match
64.1%; Score 2237.5; DB 3; Length 1107;
Best Local Similarity 60.2%; Pred. No. 3.1e-130;
Matches 441; Conservative 23; Mismatches 152; Indels 117; 357 49

GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168

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                                                                                                                                        597 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPP 656
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                                               537 GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDAGPKGADGSP
                                                                            -TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
                                                                                                                    GE----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP
                                                                                                                                                                                                       ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                            717 GAAGRVGPPGPSGNAGPPGPPGPPGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                                                                                                                 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPXGPAGERGSP
                                                                                                                                                                                                                                                                      777 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP
                                                                                                                                                                                                                                                                                           GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
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                                                                                                                                                                                                                                                                                                                                                                               GPPGP------AGPAGERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEQGVP
                                                                                                                                                              GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
                                                                                                                                                                                                                                                                                                                                      GARGOAGVMGFPGPKGAAGBPGKAGERGVPGPPGAVGPAGKDGE
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Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen, fibronectin; post translational hydroxylation; ss. transforming growth factor-betal; TGF-betal; chimera.
                                                                                   A chimeric collagen 1 (alpha1)/TGF-beta1 protein.
                                                                                                                                                                                                                          by GCT"
                      AAY84538 standard; protein; 1171 AA.
                                                                                                                                                                                                                         "Gly encoded
                                                                                                                                                                                                      Location/Qualifiers
                                                                (first entry)
                                                                                                                                                                                                                858
/note=
                                                                                                                                                                                                               Misc-difference
                                                                                                                                                           Homo sapiens.
Unidentified.
Chimeric.
                                                                25-JUL-2000
                                                                                                                                                                                                                                              EP992586-A2
                                          AAY84538
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The specification describes a method for producing an extracellular comparing the strategoration of the extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell; and the coll comparating the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-contacting the cell with a comparated into the extracellular matrix protein. The into the cell and incorporated into the extracellular matrix protein. The cert of mathod may be used to make host cells assimilate and incorporate containing the septiment of production of proteins used in the comparation of proteins used in the cell and incorporated into the extracellular matrix protein. The recombinant production of proteins used produce functional proteins depends on the post translational hydroxylation of proteins depends on the post translational hydroxylation of proteins depends on the post translational hydroxylation of proteins depende represents chimeric collagen i (alphal)/transforming the present sequence represents chimeric collagen i (alphal)/transforming method of the immediate chimer which may be produced using the cells of the immediate collagen in which may be produced using the
Claim 23; Fig 15; 260pp; English.
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Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful on

Production of extracellular

medical implants.

Х,

Connolly

Zhang G,

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Buechter

EA,

Gruskin

2000-259138/23

N-PSDB: AAA12498

(USSU) US SURGICAL

98US-00169768.

09-OCT-1998;

Sequence 1171 AA;

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                                                                                                                                                                        GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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                                                                                                                  GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPFGARGQA
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                                                                                                                                                                                                                                                           477 GSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGARGERGFPGERGVOGPPGPAGPR
                                                                                                                                                                                                                                                                                                                   537 GANGAPGNDGAKGDAGAPGAPGSOGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
                                                                                                                                                                                                                                                                                                                                                GE-----AGRPGEAGLPGAK------GLTGSPGSPGPDGKTGPPGPDGRP
                                                                                                                                                                                                                                                                                                                                                                 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                    417 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                         --TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
                                                                                                                                                                                                                                                                                                                                                                                                       GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
   Length 1171;
                              117;
                              Indels
   DB 3;
64.1%; Score 2237.5; DB 3; 60.2%; Pred, No. 3.3e-130; ive 23; Mismatches 152;
                              Conservative
 Query Match
Best Local Similarity
                              441;
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657 GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP ----VGPAGKDGEAGAGGPPGPAGP---AGERGEQGPAGSPGFGGLPGPAGPPGEAGKP

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99EP-00119184

07-OCT-1999;

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776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant nucleic acid for expressing collagen or derivatives in plants - useful as, e.g. bio-materials and in therapeutic, cosmetic and odontological compositions.
                                                                                                                                                                                                                                                                                                                                               Primer; PCR; amplification; human; collagen; mammal; plant; prosthesis; cardiac valve; ligament; tendon; skin; gingival implant; perfumes; nerve regeneration; antibiotic; growth factor; cancer; inflammatory; gelatin; glue; food.
GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGFAGEKGSP
                                                                                                       GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
                                                                                                                   GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                   GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "cleavage site for aminopeptidase"
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    .22
    /note= "signal peptide"
    .99
    /note= "mature protein"

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                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                 AAW68485 standard; protein; 1464 AA
                                                                                                                                                                                                                                                                                                                                Human recombinant collagen protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-FR002331
                                                                                                                                                                                                              GPPGPPGPPG 1029
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                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-1996;
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Bournat P;
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Peptide
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The invention relates to the production of mammalian collagen in plants. CC clones: alpha3 and alpha22, spanning the human collagen type I gene were isolated from a NG-63 osteosarcoma library. Clone alpha3 contained cover isolated from a NG-63 osteosarcoma library. Clone alpha3 contained completed from a NG-63 osteosarcoma library. Clone alpha3 contained sequence encoding amino acids are 2 clones were used to generate a number of fragments which were used to construct composite sequences encoding variant collagen molecules. The fragments are: (A) containing nucleotides (In) - 4 to 479; (B) containing crocking the pro-collagen and bases (B-77 from the sequence encoding the pro-collagen and bases (B-77 from the sequence encoding the pro-collagen and bases (B-77 from the sequence encoding the pro-collagen and bases (B-77 from the sequence encoding the pro-collagen and bases (B-77 from the sequence encoding the pro-collagen and bases (B-77 from the sequence encoding the pro-collagen and bases (B-77 from the sequence encoding the pro-collagen and bases (B-77 from the sequence encoding the pro-collagen and bases (B-77 from the sequence encoding and 1474-534) and the N-terminus of the mino propeptide domain (In 72-479); (D) all of the amino-telopeptide comain (In 72-479); (D) all of the amino-telopeptide domain (In 73-479); (D) all of the amino-telopeptide domain (In 73-479); (D) all of the central helicoidal domain (In 63-2808) of alpha22, encoding as 936-1192 in the central helicoidal domain (In 63-2808); (E) the Damilia (In 63-1464) plus stop codons, and (B) as G but the ER. This sequence represents a recombinant human collagen; (P) and (B). (E) the ER. This sequence represents a recombinant thum collagen in a shouterials (Mamostatic from fragments (A), (D), (B), (E), (E) and proteines for cardiac valves, ligaments or tendons of paramaceutical, weddical, odontological, cosmetic and biotechnological compositions (e.g. as prostheses for cardiac valves; ligaments of cultagen dystuction produced from the produce glues, 108 212 757 GVMGFPGPXGAAGEPGKAGERGVPGPPGAVGPAGXDGEAGAQGPPGPAGPAGERGEQGPA GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP---------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGFAGPKGSP GE-----AGREGEAGLEGAK-----GLIGSEGSEGFDGKIGFEGEAGDGRE GKDGVRGLTGP1GPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP 458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA Gaps Length 1464; 64.1%; Score 2237.5; DB 2; Length 1464; 60.2%; Pred. No. 3.9e-130; ive 23; Mismatches 152; Indels 117; 441; Conservative Query Match Best Local Similarity Seguence 1464 AA; 638 49 518 109 578 169 213 259 758 Matches 셤 ò g ò 엄 원 ð g ò g à

GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGAKGAGPPGATGFP 877

GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----

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GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453

878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP

----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP

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                                                                  998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 1057
                                                                                                                    1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1117
                                                                                                                                                             GPPGPPGSPGEQGPSGASGPAGPPGSPGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1177
938 GADGPAGAPGTPGPQGIAGQNGVVGLPGQRGRGFPGLPGPSGEPGKQGPSGASGERGPP 997
                                         GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses a composition comprising two or more isolated rate of human polymucleotides with the received sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates expression of a polymucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a
                                                                                               ----AGAQ 558
                                                                                                                                              GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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                                                                                           GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE
                                                                                                                                                                                                                                                                                                                                                                                              neuronal tissue; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                     Human Protein P02452, SEQ ID NO 10491.
                                                                                                                                                                                                                                                                                         ADD45059 standard; protein; 1464 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2001; 2001US-0312147P.
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26-NOV-2001; 2001US-0333347P,
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(FARB ) BAYER AG.
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spinal segmen
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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      998 GPMGPPGLAGPPGESGKEGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGV 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.1%; Score 2237.5; DB 7; Length 1464; Best Local Similarity 60.2%; Pred. No. 3.9e-130; Matches 441; Conservative 23; Mismatches 152; Indels 117; Gaps
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a ckit to perform the method, an array, a method for identifying an agent that is differentially expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the citivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polypurcleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (cc) spin and spared nerve injury (CNI) in an animal (e.g. gene the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed printed in the function in the sequence of the sequence of the part of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                        Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Costigan M;
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                                                                                                                                                            Human Protein P02452, SEQ ID NO 10487
                   ADD45055 standard; protein; 1464 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                               (first entry)
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(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Woolf C, D'urso D,
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                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                             29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-2003.
                                                                  ADD45055;
ADD45055
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Query Match 64.1%; Score 2237.5; DB 7; Length 1464; Best Local Similarity 60.2%; Pred. No. 3.9e-130; Matches 441; Conservative 23; Mismatches 152; Indels 117; Gaps 12;

998 GPWGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 1057 1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1117 1118 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLMGLPGPIGPPGPRGRTGDAGPV 1177 454 GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP 258 698 GANGAPGNDGAKGDAGAPGAPGSQGAPGLYQGMPGERGAAGLPGPKGDRGDAGPKGADGSP 757 GE----AGRPGEAGLPGAK-----GLIGSPGSPGPDGKIGPPGPAGDGRP 300 ----VGPACKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393 878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937 394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453 559 GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603 169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP-------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 301 GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. Human Protein P02452, SEQ ID NO 10483. ADD45051 standard; protein; 1464 AA. 1178 GPPGPPGPPGPPG 1190 604 GDLGAPGPSGPAG 616 (first entry) WO2003016475-A2 GPP-29-JAN-2004 Homo sapiens 27-FEB-2003 213 342 Н 49 109 638 ADD45051; 259 RESULT 11 유 g 원 임 g ò ò ď ò 9 8 ò ò δ ò 원 ò D Ωþ ð 8 à

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1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPRGDKGETGEOGDRGIKGHRGFSGLQ 1117
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                                                                                                                                                          818 GADGQPGAKGEPGDAGAKGDAGPPGPPGPIGNVGAPGAKGARGSAGPPGATGFP 877
                                                                                                                                                                                                                                                    878 GAAGRVGPPGPSGNAGPPGPPGFAGKGGKGPRGETGPAGRPGEVGPPGPPGPPGFAGKSP 937
                                                                                                                                                                                                                                                                                                                             GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
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/note= "Encoded by ggcgaacctggtgatgctggtgctaaaggcgatg
ctggtcccccggccctgctgga"
--GLTGSPGSPGPDGKTGPPGPAGQDGRP
                                                 758 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP
                                                                                                           301 GPPGPPGARGQ------AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---
                                                                                                                                                                                                                    ----VGPAGKDGEAGAQGPPGPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
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  GE------AGRPGEAGLPGAK---
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10-NOV-2000; 2000US-00709700.
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N-PSDB; AAD06576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence which is differentially required in a naimal subjected to pain and a latt to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of a polynucleotide sequence which is differentially subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in na naimal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating specification, a method for identifying a compound useful in treating of pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CMI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form mark of the printed sequence data for this patent did not form mark of the printed sequence data for this patent did not form mark of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               698 GANGAPGUDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGFKGDRGDAGPKGADGSP 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                        composition comprising two or more isolated polypeptides, useful for baring a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.1%; Score 2237.5; DB 7; 60.2%; Pred. No. 3.9e-130; ive 23; Mismatches 152;
                                                                                                                                                                                                                                                    Costigan M;
                                                                                                                                                                                                                                                 Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 1017pp; English.
                                                    14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
  14-AUG-2002; 2002WO-US025765
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Best Local Similarity 60.29
Matches 441; Conservative
                                                                                                                                                                (GEHO ) GEN HOSPITAL CORP
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                     preparing a medicament
                                                                                                                                                                                                                                                                                                      WPI; 2003-268312/26.
GENBANK; P02452.
                                                                                                                                                                                                                                                 Woolf C, D'urso D,
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us-10-658-989a-2.rag

The present sequence is porcine alphal(I) collagen. The present invention relates to recombinant synthesis of collagens and gelatins derived from animals. Collagen is useful in medical, pharmaceutical, food and cosmetic industries. Collagen is useful in medical, paramaceutical, food and cosmetic incontinence implants, and for treating autoimmune disorders such as rheumatoid arthritis. Collagen is useful in food products such as sausage casings, and in cosmetics or facial and skin products such as sausage asings, and in cosmetics or facial and skin products such as sausage casings, and in cosmetics or facial and skin products such as sausage molisturisers. Recombinant gelatin is useful in vacious pharmaceutical and medical devices and products, in food and beverage industries, in hair medical devices and products, in food and beverage industries, in hair manufacturing processes, as a light-sensitive coating in various electronic devices, as photoresist base in photolithographic processes, in printing and photographic applications, in laboratory application, and as a component in various gels used for biochemical and electrophoretic analysis, including enzymographic gels and for treating autoimmune disorders, infections and cancer Example 3; Fig 8; 168pp; English.

Sequence 1449 AA;

13; RGERGFPGLPGPSGEPGKQGPSGERGPPGPMGP---PGLAGPFGESGREGAPGAEGS 1008 365 482 531 120 180 RGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPAGERGE 572 GEAGLPGAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGPPGARGQAGVMGFPGPKGAA 591 GPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAK 711 --TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----A 261 GPPGPAGAPGDKGETGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGOPGAKGGP 831 TGPPGPIGSVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPAGKEGS 891 ---RGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGP 422 KGPRGETGPAGRPGEAGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQRGVVGLPGQ 951 9 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP GARGEPGPAGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA ---PGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPPGPAGEA PGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGS P---GSPGPD---GKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGE GRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGP---PGPPGARGQAGVMGF-Indels 94; Gaps Length 1449; GPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP-64.0%; Score 2234; DB 4; 162.0%; Pred. No. 6.4e-130; ive 21; Mismatches 154; Query Match Best Local Similarity 62.0% Matches 438; Conservative 1009 472 532 121 592 181 652 213 712 772 318 892 423 952 262 832 366 483 537 ઠે g 원 g d ò 셤 g d ò ò g ò $\stackrel{>}{\circ}$ ઠે ò Db à ò qq

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New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer or non-cancerous disease states of the pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to novel nucleic acids and proteins present in normal and neoplastic pancreatic cells. Pancreatic cancer is a common cause of cancer death worldwide, therefore accurate methods of diagnosis and treatment are required. Compounds which modulate the proteins of the invention may have cytostatic activity and the protein and DNA sequences of the invention may be useful for the development of a vaccine or in gene therapy. The composition and methods are useful in diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer and non-cancerous disease states of the pancreas. The present sequence is that of a human pancreatic protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGPPGARGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.0%; Score 2233.5; DB 7; Length 1161; 60.0%; Pred. No. 5.7e-130; ive 23; Mismatches 153; Indels 117;
                                                                                                                                                                                                                                                                  cell; pancreatic cancer;
                      573 QGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----
                                                                                                                                                                                                                              Human pancreatic cell protein sequence SegID510.
                                                                                                                                                                                                                                                                                 cancer death; cytostatic; vaccine; gene therapy non-cancerous pancreas disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; SEQ ID NO 510; 635pp; English
                                                                                                                                                                                                                                                                  cell; pancreatic
                                                                                                                       Æ
                                                                                                                      ADE87050 standard; protein; 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-2002; 2002WO-US040655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-2001; 2001US-0342768P
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                                                                                                                                                                                                                                                                  pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DIAD-) DIADEXUS INC.
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Best Local Similarity
Matches 440; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADE87387
                                                                                                                                                                                                                                                                                                                                                                       WO2003060145-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C;
                                                                                                                                                                                                                                                                                                                                       Ното варіелв.
                                                                                                                                                                                             29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                         24-JUL-2003
                                                                                                                                                                                                                                                                  neoplastic
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                                                                                                                                                           ADE87050;
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                                                                                                                                                                                                                                                                                                                                                      814
                                                                                                                                                                                                                                                                                                                                                                                           815 GPPGPPGSPGEQGPSGASGPAGPPGSAGAPGKNGLNGLPGPIGPPGPRGRIGDAGPV 874
GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR 394
                                                                                                                                                                                                                                                   635 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP 694
                                                                                                                                                                                                                                                                                            GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP
                                                                                      GADGOPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP
                                                                                                                                                                           ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                 575 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                                                                                                                                            GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                                                                                                                                                                                                                    GPAGKSGDRGETGPAGPAGPVGPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ
                                                                                                                                                                                                                                                                                                                                                                              GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP
                                                                                                                         GPPGPRGARGO-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---
                                                                                                                                                                                                                           GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                         -TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, deer, rat, mouse, DACC, deer antler cartilage cell; cell stimulation; cell inhibition; cell growth; cell division; mesenchymal cell; chondrocyte; chondrogenesis; osteogenesis; growth; repair; regeneration; restoration; extracellular marrix; cartilaginous matrix; cartilage; disc; connective tissue; agonist;
                                                                                                                                                                                                                                                                                                                              GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide orthologous to DACC-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG93947 standard; protein; 1461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPPGPPGPPGPPG 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonist; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                 GDLGAPGPSGPAG
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The invention discloses a method for stimulating or inhibiting cell growth and/or division which comprises contacting or inserting into an animal cell a polypeptide comprising one of the deer antler cartilage cell (DACC) clones disclosed. More particularly, the method relates to these polypeptides stimulating mesenchymal cell growth and/or division and to transfecting these cells and chondrocytes with vectors carrying the genes of these polypeptides capable of stimulating chondrogenesis, osteogenesis, growth, repair, regeneration and/or restoration of the certacellular matrix. The chondrocytes selectively express genes required to form a cartilaginous matrix. The DACC polypeptides and polynucleotides are useful for identifying an agent that modulates the activity of the polypeptide, for stimulating mesenchymal cells growth and/or division by exposing animal mesenchymal cells to conditioned media or its active growth and/or division by inserting into an animal cell, a compound which inhibits the translation of the polynucleotide encoding the DACC. The method and the polypeptides are useful for stimulating mesenchymal cell growth midlo or division of the polynucleotide encoding the DACC. The inhibits the translation of the polynucleotide encoding the DACC. The conditions of the polynucleotide encoding the method and antagonists and animal. The polynucleotides, polypeptides, agonists and antagonists or animal. The polynucleotides, polypeptides, agonists and antagonists of dentify other proteins, which bind to or interact with the polynucleotides and are involved in modulating cell growth and/or division.

The sequences presented in ABG99923-ABG99848 are the proteins encoded by the DACC cDNA clones Stimulating or inhibiting cell growth and/or division, useful for stimulating chondrogenesis, cartilage, disc or connective tissue growth, repair, and/or regeneration, comprises administering deer antler Claim 13; Page 154-160; 214pp; English cartilage gene

Sequence 1461 AA;

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514 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 634 258 754 755 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP 814 341 342 -----VGPAGKUGEAGAQGPPGPAGP---AGERGEQGPAGSPGFPGGLPGPAGPPGEAGKP 393 394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453 GSPGFQGLPGPAGPPGBAGKPGBQGVPGDLGAPGPSGARGBRGFPGBRGVQGPPGPAGPR ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPKGSP GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 515 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP----GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----Length 1461; Indels 64.0%; Score 2233.5; DB 5; 60.0%; Pred. No. 6.9e-130; ive 23; Mismatches 153; 64. 60.08; Find GPPGPPGARGQ------Query Match Best Local Similarity 60.0 Matches 440; Conservative 9 109 575 635 695 301 875 169 213 259

> 15-FEB-2001; 2001AU-00003116. L5-FEB-2002; 2002WO-AU000163

(ADPP-) ADP PHARM PTY (UNSY) UNIV SYDNEY.

WPI; 2002-643456/69.

Ghosh P;

Roubin R,

levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as contraceptive, treating osteoporosis and osteoarthritis, anaemia, allabelmer's Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allargy, asthma, graftversus-host disease, ecema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention

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The invention relates to polynucleotides encoding novel human proteins or raised against the polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight are used to identify compounds which bind to the polypeptides are used to identify compounds which bind to the polypeptides or below of polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulgant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporossis; tissue regeneration; immune disorder.
GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                      GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGPV
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                                                                                                                                                                                                                                                  GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES	ΩΙ	US-09-331-347C-21	3-963-825-1	US-09-500-811-18	US-09-570-573-18	US-09-548-608-18	US-09-585-887-9	US-09-289-578-9	0	US-09-219-849-49	US-08-468-996-10	US-08-931-820-3	US-08-963-825-20	US-09-010-999-1	US-09-500-811-20	US-09-570-573-20	US-09-548-608-20	US-08-316-650-12	PCT-US95-02251-12	4	US-09-219-849-50	-642-25	-08	-09-219-84	US-08-642-255-53	US-08-963-825-21	US-09-500-811-21	US-09-570-573-21
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US-09-548-608-21	US-08-931-820-2	US-08-963-825-19	US-09-500-811-19	US-09-570-573-19	US-09-548-608-19	US-09-585-887-10	US-09-289-578-10	US-08-642-255-72	US-09-219-849-5	US-08-468-996-12	US-09-919-497-56	US-08-642-255-132	US-08-397-633A-53	US-08-175-155-68	US-08-477-509B-103	US-08-642-255-101	US-08-707-237A-75
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ALIGNMENTS

21, Application US/09331347C 56.17431 INFORMATION: THE Maristem Therapeutics, S.A. THE Maristem Therapeutics, S.A. THE Moristem Therapeutics, S.A. THE Moristem Therapeutics, S.A. THE MORISTEM THE	64.1%; Score 2237.5; DB 4; Length 1464; larity 60.2%; Pred. No. 1.2e-133; Conservative 23; Mismatches 152; Indels 117; Gaps 12;	GPPGEPGFTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48	GPKGSPGBAGRPGBAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108 	GVMGFPGPKGAAGEPGKAGERGVPGPPAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 	GSPGFQGLPGFAGPPGEAGKPGEQGVPGDLGAPGPSGFAGEPGP 212 	TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP 258	GEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGFAGDGRP 300 	GPPGARGQ341 -
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Carrying Out to the Presence of
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                                                                                                                                                                                                                                                                       GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                           GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGBRGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                 454 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAOGPPGPAGPAGERGEOGPA 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       874 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAXGAXGAPGPV 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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                                                                                                     Length 1341;
                                                                                                                                                117;
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A Method for Assaying Collagen Fragments

in Body Fluids, A Test Kit and Means for

Method and Use of the Method to Diagnose

Disorders Associated with the Metabolism
                                                                                                   63.9%; Score 2228.5; DB 3; Length 60.0%; Pred. No. 4.2e-133; ive 23; Mismatches 153; Indels
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                 IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1
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                                                                                                     Query Match
Best Local Similarity 60.0°
Matches 440; Conservative
    Homo sapiens
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                                              ; CLONE: CC
US-08-963-825-18
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US-09-500-811-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Qvist, Per APPLICANT: Qvist, Per APPLICANT: Qvist, Per APPLICANT: Qvist, Martin TITLE OF INVENTION: A Method for Assaying Collagen Fragments TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out tITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                    1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1117
                                                                         GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937
                                                                                                                                                                                                         GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                                                                                                                       394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
                                                                                                                                                                                                                                                                                                                                                                             GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 877
                                                                                                                                                               938 GADGPAGAPGTPGPQGIAGORGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP
                                          ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                           511 GARGOAGVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION UNDER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGEN INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELEPHONE: 212-527-770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,714
29,714
775. 4305/08701
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US-08-963-825-18
US-08-963-825-18
Sequence 18, Application US/08963825
Patent No. 6110689
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PEDIUM TYPE: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 1341 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 GDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH:
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COUNTRY: USA

COMPUTRY: USA

ZIP: 10022
COMPUTER READELS FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
FLING DATE:
CLASSIFICATION NUMBER: US/09/570,573
FLING DATE:
APPLICATION NUMBER: US/09/570,573
FLING DATE:
APPLICATION NUMBER: US/09/570,573
FLING DATE:
ATORNEY AGENT INFORMATION:
NAME: GOGOTIS, Adda C.
REFERENCE/DOCKET NUMBER: 4305/08701
TELECHONE: 212-527-7700
TELECHONE: 212-527-7700
TELECHONE: 212-527-7700
TELECHONIN: 212-527-7700
TELECHONE: 212-527-7700
TELECHONE: ALSO TON: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
TYPE: Amino acid
TOPOLOGY: linear
MOLECULE TYPE: PROTECH:
ORIGINAL SOURCE:
OCALNISM: HOMO SADIENS
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IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1
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US-09-570-573-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514 GSPGFPQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 GSPGFOGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 ------TGLPGPPGERGCPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.9%; Score 2228.5; DB 3; Best Local Similarity 60.0%; Pred. No. 4.2e-133; Matches 440; Conservative 23; Mismatches 153;
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby PC
STRET: New York
CITY: New York
COUNTRY: New York
COMPUTRY: USA
ZIP: 10022
COMPUTR: BEADABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTR: BAPCONDENCE FLODS/MS-DOS
SOFTWARE: PATCHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHING SYSTEM: PSPLICATION NUMBER: US/09/500,811
FILING DATE:
TELEPHONE: 212-73-700
TELEPHONE: 212-73-6237
TELEX: 216687
TELEX: 216687
TELEX: 2141 Animo acids
WANTHER TABLESTICS:
SEQUENCE CHARACTERISTICS:
SUMBING: Laboration acids
WANTHER TABLESTICS:
SUMBING: Laboration acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: COLLAGEN ALPHA 1 (I)
US-09-500-811-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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510 453 ---- AGAQ 558 559 GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603 GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-----

Sequence 18, Application US/09570573

Sequence 18, Application US/09570573

Sequence 18, Application US/09570573

Sequence 18, Application US/09570573

GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Goode, Martin
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: Bos Third Avenue
CITY: New York

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Tue Oct 19

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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: 1 ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-548-608-18
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Matches 440;
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Sequence 18, Application US/09548608
Patent No. 6355422
GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: Goale, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              994 GPPGPPGSPGEPGGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGP1GPPGPRGRTGDAGPV 1053
                                                                                                                                                                            GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAQQDGRPGPPGPPGARQQA 453
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                                                                                                                                                                                                                  GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA. 168
                                                                                                                                                                                                                                                                            GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP---- 212
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                                                                                                                      334 GPPGPAGEEGKRCARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                    GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
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                                                               Gaps
                              Length 1341,
                                                            Indels 117;
                                  DB 3;
                              tch 63.9%; Score 2228.5; DB 3; al Similarity 60.0%; Pred. No. 4.2e-133; 440; Conservative 23; Mismatches 153;
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                             Query Match
Best Local S:
Matches 440
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                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                            APELICATION NOMBER: US/US/S46,005
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION UNDER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: QSQUIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/087
TELEBRANE 212-57-7700
TELEBRANE: 212-57-7700
TELERAX: 212-57-7700
TELERAX: 212-57-7700
TELERAX: 212-57-7700
TELERAX: 216-687
INFORMATION FOR SEQ ID NO: 18:
SEQUIENCE CHARRATERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                               E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
STREET: 805 Third Avenue CITY: New York STATE: New York COUNTRY: USA
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                                                                                                           ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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TB-7-800-000-0T-8D

259 , 755 , 301 , 342 , 342 , 342 , 342	Db 935 GADGPAGAPGIPGPQGIAGQXGVVGLFGGFFFGLFGFSGEFGAQGFSGAGGFFFF 791 Qy 454 GPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510 Db 995 GPMGPPGLAGPPGESGREGSPGRDGSPGAKGBRGBTGPAGPPGAPVAPGPV 1054 Qy 511 GARGAGVWGFPGPKGAAGEPGKAGSRGVPGPPGAVQPAGKDGEAGAQ 558 Db 1055 GPAGSGGRGETGPAGAPAGRAGARGAPGAPAGAPGAPVAPGBV 1014	QY 559 GPPGPAGPAGERGEOGPAGSPGFQGLPGPAGPPGEAGKPGEOGVP 603 Db 1115 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPFGPRGRTGDAGPV 1174 QY 604 GDLGAPGPSGPAG 616 Db 1175 GPPGPPGPPG 1187 RESULT 7 US-09-289-578-9	sequence 9, Application US/092895/8 Sequence 9, Application US/092895/8 GENERAL INFORMATION: APPLICANT: Chang, Robert APPLICANT: Hargen APPLICANT: Chang, Robert APPLICANT: Chisholm, George TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND TITLE OF INVENTION: USUGATE TITLE OF INVENTION: CELLS. TITLE OF INVENTION: CELLS. TITLE OF INVENTION: CELLS. CORRENCE: 225002030400 FILE REFERENCE: 225002030400 CORRENT APPLICATION NUMBER: US/09/289,578	PRICE APPLICATION NUMBER: 60/084,828 PRICE FILING DATE: 1998-05-08 NUMBER OF SEQ ID NOS: 11 SEQ ID NO 9 LENGTH: 1461 TYPE: PRICE CREANISM: Homo sapiens US-09-289-578-9	Query Match 63.8%; Score 2224.5; DB 4; Length 1461; Best Local Similarity 59.9%; Pred. No. 8e-133; Matches 439; 117; Gaps 12; Qy 1 GPPGEDGPTGLPGPPGERGGPGSRGFPGADGRAGERGSPGPA 48 11
Qy 394 GEOGVPGDLGAPGEPGEPGERGGESRGFPGADGVAGPKGPAGERGSP 453 Db 814 GADGPAGAPGTPGLAGQRGVVGLPGQRGBRGFPGLPGPSGEPGKQGPSGASGERGPP 873 Cy 454 GPAGPKGSPGBAGRPGEPGLPGARGITGSPGSPGPPGAGGDGRRGPPPGPP 873 Cy 454 GPAGPRGSPGBAGRPGBAGLTGSPGSPGBAKGDRGPPAGGDGRRGPPPP 510 Db 874 GPMGPPGLAGPPGESGREGAPGABGSPGRAGBRGAKGDRGBTGPAGPBACACABACGPP 933 Qy 511 GARGQAGVWGFPGPAGABPGRAGBRGVGPAGPAGPAGPAGDRGTAGHAGFSGLQ 993 Db 934 GPAGKSGDRGTGPAGABPGARGRAGBAGPAGPAGPAGDRGTKGHRGFSGLQ 993 Qy 559 GPPGPAGPAGERGEQCPAGSP	Db 994 GPPGPPGSPGGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGFRGRTGDAGPV 1053 Qy 604 GDLGAPGPSGPAG 616 Db 1054 GPPGPPGPPG 1066 RESULT 6	Sequence 9, Application US/09585887 Sequence 9, Application US/09585887 Sequence 9, Application G413742 GENERAL INFORMATION: APPLICANT: Chang, Robert APPLICANT: Chang, Robert APPLICANT: Hitzeman, Ronald A. APPLICANT: Hitzeman, Ronald A. APPLICANT: Hitzeman, Ronald A. TITLE OF INVENTION: WOVEL WETHODS FOR THE PRODUCTION OF GELATIN AND TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT TITLE OF INVENTION: CELLS FILE REPERENCE: 228002030400	CURRENT APPLICATION NUMBER: US/09/585,887 CURRENT FILING DATE: 2000-05-31 FRIOR APPLICATION NUMBER: 09/289,578 PRIOR APPLICATION NUMBER: 09/289,578 PRIOR PAPLICATION NUMBER: 60/084,828 FRIOR PAPLING DATE: 1998-05-08 NUMBER OF FILING DATE: 1998-05-08 SEQ ID NOS: 11 SEQ ID NO 9 LENGTH: 1461 TYPE: PRT CRANISM: Homo sapiens US-09-585-887-9	Query Match 63.8%; Score 2224.5; DB 4; Length 1461; Best Local Similarity 59.9%; Pred. No. 8e-133; Matches 439; Conservative 23; Mismatches 154; Indels 117; Gaps 12; Qy 1 GPPGERGPTGLPGPPGERGGPGSRGPPGADQAGPRGPRGPAGERGSPGPA 48	109 GWGFPGPKGAAGEPGKAGERGVPGPGAVGPAGKTGFPGPAGQDGRPGPPGPPGP 109 GWGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKTGFPGPAGQDGRPGPPGP 109 GWGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGE 169 GSPGFQGLPGPAGEPGKPGEQGVPGDLGAPGFSGPAGE 169 GSPGFQGLPGPPGBAGKPGEQGVPGDLGAPGFSGPAGE 169 GSPGFQGLPGPAGPPGAKPGEQGVPGDLGAPGPSGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG

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                                                                           63.3%; Score 2208.5; DB 3; Length 1057; 60.3%; Pred. No. 6.2e-132; ive 23; Mismatches 158; Indels 105;
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Patent No. 6150081
GENERAL INFORMATION:
APPLICANT: VAN HERNE, GEORGE V.
APPLICANT: WAN RIAN, ALEXIS C.
APPLICANT: BOUNGTRA, JAN B.
APPLICANT: BOWOLF, FREDERIK A.
APPLICANT: WOORRORK, ANDREAS
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WERTEN, MARC W.T.
     Homo sapiens
3: Collagen type
                                                                                                                435; Conservative
                                                                             Query Match
Best Local Similarity
Matches 435; Conserv
   ) ORGANISM: Hor
; TISSUE TYPE:
US-08-931-820-1
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US-09-219-849-49
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                                                                                                                                                                                                           394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
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GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 634
                                                                       GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR 694
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                                                                                                                                                                                                                                                                                                                                     342 ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
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                                                                                                                                                  GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
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                                                                                                            ------TGLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSPGPAGPKGSP
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OUMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (E
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
                                     GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
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US-08-931-820-1
; Sequence 1, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
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STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
FILE REPERBINCE: 2728-2728-CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT APPLICATION NUMBER: 1998-12-23
SOFTWARE: PATENTING DATE: 1998-12-23
SOFTWARE: PATENTIN VOY: 50
SOFTWARE: PATENTIN VOY: 2.1
                                                                                                                                                                                                                                                                                                                       1 GPPGEPGPTGLPGPPGE------RGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                              Score 2191; DB 3; Length 822;
Pred. No. 6.3e-131;
2; Mismatches 158; Indels 150;
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Best Local Similarity 56.9%; Pre
Matches 436; Conservative 22;
                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                         ; OTHER INFURNA
US-09-219-849-49
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                                                                                                                                                                                                                            DIABETES
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OSCUENCE 10, Application US/08468996
Patent No. 645504
GENERAL INFORMATION:
APPLICANT: Wainer, Howard
APPLICANT: Wainer, Ariel
APPLICANT: Miller, Ariel
APPLICANT: Abmad, Al-Sabbagh
TITLE OF INVENTION: GLUCAGON
FILE OF INVENTION: GLUCAGON
FILE REFERENCE: 1010/16959-US3
CURRENT APPLICATION NUMBER: US/08/468,996
CURRENT FILING DATE: 1990-02-21
PRIOR PILING DATE: 1990-02-21
PRIOR PILING DATE: 1990-10-15
PRIOR PILING DATE: 1990-10-16
PRIOR PILING DATE: 1990-10-16
PRIOR PILING DATE: 1990-10-16
PRIOR PILING DATE: 1990-10-17
PRIOR PILING DATE: 1990-10-17
PRIOR PILING DATE: 1990-07-10
PRIOR PILING DATE: 1990-07-11
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US-08-468-996-10
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Sequence 20, Application US/08963825;
Patent No. 6110689
Patent No. 6110689
GENERAL INPORMATION:
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
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TITLE OF INVENTION: Disorders Associated with the Metabolism of TITLE WITH THE METABOLISM OF TITLE WITH
                                                          164 GNDGQPGPAGPPGPVGPAGGPGFPGAPGARGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 223
                                                                                                               -----GKDGEAGAQGPPGPAGPRGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
                                                                                                                                              224 GASGNPGIDGIPGAKGSAGAPGIAGAPGFPGPRGPPDPQGATGPLGPKGQTGKPGIAGFK 283
                                                                                                                                                                                                                                                GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 GRPGPPGPPGPQPGVMGFPGFKGANGEPGKAGEKGLPGAPGLRGLPGKDGETGAEGPP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 GPAGPAGERGEQGAPGPSGFQGLPGPPGEGGKPGDQGVPGEAGAPGLVGPRGERGFP 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------PGPTGLP-----GPPGERGGPGSRGPPGADGVAGPKGPA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 GDRGDVGEKGPEGAPGKDGGRGLTGPIGPPGPANGEKGEVGPPGPAGSAGARGAPGER 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               644 GETGPPGTSGIAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 703
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                                                                                                                                                                                                                    GD---LGAPGPSGPAGEPGPTGLP------GPPGERGGPGSRGFPGADGVA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 616
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        GQDGRPGPPGPRGARGQAGVMGFP-
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FILING DATE:
CLASSIFICATION: 436
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US-08-963-825-20
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565 GDRGDVGEKGPEGAPGAPGLTGPIGPPGPAGANGEKGEVGPPGPAGSAGARGAPGER 624
                                                                                   GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
                                                                                                                                      445 GPAGPAGERGEQGAPGPSGFQGLPGPPGPPGBAGKPGDQGVPGEAGAPGLVGPRGERGFP 504
                                                                                                                                                                                           -----GPPGERGGPGSRGFPGADGVAGPKGPA 447
                                                                                                                                                                                                                          505 GERGSPGAQGLQGPRGLPGTPGTPGPKGASGPAGPPGAQGPPGLQGMPGERGAAGIAGPK 564
                                                                                                                                                                                                                                                                                                -----AGRPGEAGLPGAKGLTGSPGSPGPD 489
                                                                                                                                                                                                                                                                                                                                                                                                                                         GERGVPGPPGA-----VGPAGKDGEAGAQGPPGPA---GPAGERGEQGPAGSPGFQ 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               685 GARGAQGPPGATGFPGAAGRVGPPGSNGNPGPPGPPGPSGKDGPKGARGDSGPPGRAGEP 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
FLING APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assay for collagen degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616
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                                                                                                                                                                                                                                                                                                GERGSPGPAGPKGSPGE -----
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US-08-931-820-3
5 Sequence 3, Application US/08931820
7 Patent No. 6010863
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Collagen type II
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amino acid
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Best Local Similarity 52.1%
Matches 393; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 amino aci
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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TISSUE TYPE:
US-08-931-820-3
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                                                                                   358
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--GPKGAAGEPGKAGERGVPGPPGAVGPA 141
816 GARGAQGPPGATGFPGAAGRVGPPGSNGNPGPPGPPGPSGKDGPKGARGDSGPPGRAGEP 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                        APPLICANT: Poole, Anthony R.
APPLICANT: Poole, Anthony P.
APPLICANT: Hollander, Anthony P.
APPLICANT: Hollander, Anthony P.
TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.7%; Score 1943; DB 3; Length 1418; Best Local Similarity 52.1%; Pred. No. 4e-115; Matches 393; Conservative 34; Mismatches 189; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 583 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 616
                                                                            876 ĠĽQĠPAĠPPĠEKĠEPĠDDĠPSĠAEĠPPĠPQĠLAĠ 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Human Type II Collagen
US-09-010-999-1
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  RESULT 13
US-09-010-999-1
Sequence 1, Application US/09010999; Patent No. 6132976
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEFHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1418 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: 1:---
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55.7%; Score 1943; DB 3; Length 1418;
Best Local Similarity 52.1%; Pred. No. 4e-115;
Matches 393; Conservative .34; Mismatches 189; Indels 138;
                                                                                NAME: GGGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET UNMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
INMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                            TELEX: 236687
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1418 amino acids
                                                                                                                                                                                                                                                      : 1418 amino acids
amino acid
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                            linear
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TOPOLOGY:
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US-08-963-825-20
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                                                        29,714
3R: 4305/08701
                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                    NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-527-7700
TELEFAX: 212-527-7700
TELEX: 236687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 LENGTH: 1418 amino acids
                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09500811
Patent No. 632314
GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for
TITLE OF INVENTION: Method and Use of the Method to Diagnose of TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
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ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-500-811-20
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GPAGPAGERGEQGPAGSPGFPGGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        756 GETGÉPGTSGIAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 815
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336 GASGNPGTDGIPGAXGSAGAPGIAGAPGFPGPRGPFDPQGATGPLGPXGQTGKPGIAGFK 395
                                                                                                                                                             -----PGPTGLP------GPPGERGGPGSRGFPGADGVAGPKGPA
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                                                          ------GPPGERGGPGSRGFPGADGVA
                                                                                396 GEQGPKGEPGPAGAPQAPGBAGEEGKRGARGEPGGVGPIGPPGERGAPGNRGFPGCDGLA
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                                                                                                                                                                                                             GREGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP
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                                                            GD---LGAPGPSGPAGEPGPTGLP----
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                                                                                                                           Sequence 20, Application US/09570573

Bequence 20, Application US/09570573

Bedent No. 6342361

GENERAL INFORMATION:

APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNDGQPGPAGPPGPVGPAGGPGPPGARGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/570,573
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.7%; Score 1943; DB 3; 52.1%; Pred. No. 4e-115; iive 34; Mismatches 189;
                            876 GLOGPAGPPGEKGEPGDDGPSGAEGPPGPDGLAG 909
            583 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4305/08701
                                                                                                                                                                                                                                                                                                                          STREET: Darby & Darby PC STREET: 805 Third Avenue CITY: New York COUNTRY: USA ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REPREBNCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 236697
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 1418 amino acids
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Matches 393; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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US-09-570-573-20
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1 LEG OCC 17 07.17.10 400

OM protein - pro Run on: Title: Perfect score: Sequence: Scoring table:	Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on: October 18, 2004, 13:42:06; Search time 79:3776 Seconds (without alignments) 2513.149 Million cell updates/sec Title: US-10-658-989A-2 Perfect score: 3488 Sequence: 1 GPPGEPGPTGLPGPPGERGGGEQGVPGDLGAPGPSGPAGG 617 Scoring table: BLOSUM62 Gapop 10:0, Gapext 0.5
Searched:	1360919 segs, 323318874 residues

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Published Applications AA:*

(cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	2237.5	:	1057	151	US-10-104-889-20	Sequence 20, Appl
1 73	2237.5	64.1	1107	15	US-10-104-889-11	11
m	2237.5		1171	15	US-10-104-889-8	ω,
4	2237.5		1388	15	US-10-104-889-10	Sequence 10, Appl
Ŋ	2237.5		1464	14	US-10-216-705-21	
9	2237.5		1464	16	US-10-357-851-1	Sequence 1, Appli
7	2237.5		1464	16	US-10-358-024-1	Sequence 1, Appli
œ	2237.5		1464	17	US-10-788-792-150	Sequence 150, App
6	2234		1449	15	US-10-402-089-8	Sequence 8, Appli
10	2234		1449	15	US-10-402-072A-8	Seguence 8, Appli
11	2233.5		1461	16	US-10-468-091-25	Sequence 25, Appl
12	2233.5		1464	14	US-10-291-265-243	Seguence 243, App
13	2231.5	64.0	1057	15	US-10-104-889-16	Sequence 16, Appl
14	2228 5		1341	14	US-10-058-124-18	Sequence 18, Appl

Sequence 261, App Sequence 159, App Sequence 36, Appl Sequence 2, Appl Sequence 65, Appl Sequence 65, Appl	equence 79 equence 2, equence 2, equence 6,	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	404441 80 -44704	Sequence 17, Appl Sequence 17, Appl Sequence 50, Appl Sequence 12, Appl Sequence 12, Appl Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli
US-09-918-715- US-10-060-036- US-10-171-311- US-10-1749-352-	US-10-301-02-7 US-10-402-084-7 US-10-402-08-0 US-10-104-889-6 US-10-468-091-2	US-10-342-331 US-10-639-286 US-10-194-441 US-10-058-124 US-10-468-091	US-10-194-441A-10S-10-468-091-6 US-10-233-885-4 US-10-231-581-4	US-10-23-17 US-10-343-17 US-10-342-33 US-10-342-33 US-10-402-08 US-10-402-08 US-10-402-08 US-10-402-08
44664 44664 11111	446666	822 1 0017 1 0014 1 1 4 1 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7487 7144 7144 1144 1144 1144	562 5901 5901 1466 1466 1466 1566 1566 1566 150 1666 1666 170 180 180 180 180 180 180 180 180 180 18
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ALIGNMENTS

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US-10-104-889-20

Sequence 20, Application US/10104889

PUBLICATION NO. US20040086561A1

GENERAL INFORMATION:

BROKAW, JANE

BROKAW, JANE

BROKAW, JANE

BROKAW, JANE

TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSE: DIMORTH & BARRESE

STREET: 33 EAALE OVINGTON BOULEVARD

CITY: UNIONDALE

STATE: NY

COUNTRY: U.S.A.

ZIP: 11553

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PARALE STAM: COMPATE:

COMPUTER: BLANCALON DATA:

APPLICATION NUMBER: US/10/104,889

FILING DATE: 22-MAR-2005

CLASSIFICATION NUMBER: US/09/169,768

FILING DATE: 10-1098

ATTORNEY/AGENT INPORMATION:

MAME: STEEN, JEFREY S

TELECRAMMUICATION INPORMATION:

MADE: STEEN, JEFREY S

TELECRAMMUICATION INPORMATION:

TELEBRAX: (516) 228-8484

TELEFAX: (516) 228-8516
RESULT 1
US-10-104-889-20
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                                                                                                                                                                                                                                                        108
                                                                                                                                                                                                                                                                                                                                297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
                                                                                                                                                                                                                                                                      168
                                                                                                                                                                                                                                                                                                                                                                      GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP---- 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---- 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     717 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
                                                                                                                                                                                                                                                   49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                           GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                 477 GSPGFQGLPGPAGPPGEAGKPGBQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   657 GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGPP
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                                                                                                                                                                   Gaps
                                                                                                                                     DB 15; Length 1057;
                                                                                                                                Query Match
Best Local Similarity 60.2%; Pred. No. 1.9e-104;
Matches 441; Conservative 23; Mismatches 152; Indels 117;
                                                         TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GPPGPPGARGQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.1%; Score 2237.5; DB 15; Length 1107; Best Local Similarity 60.2%; Pred. No. 2e-104; Aatches 441; Conservative 23; Mismatches 152; Indels 117; Gaps
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                                                                                            ADDRESSEE: DIIWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEMP PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Ver
SOFTWARE: PETENTIN DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/169,768
ATTORNEY/AGENT INFORMATION:
NAME: STEEN
NAME: STEEN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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;
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-104-889-11
                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
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----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393

342

Sequence 11, Application US/10104889; Publication No. US20040086961A1; GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.; BUECHTER, DOUGLAS;

RESULT 2 US-10-104-889-11

qa	717 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 776	<i>&</i>	1 GPP
ò	394 GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGBRGGPGSRGFPGADGVAGPKGPAGERGSP 453	qu ·	297 GPPGPAGE
qq	777 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGERGFPP 836	ò	49 GPKGSPGE
ò	454 GPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510	qq	357 GPKGSPGE
DÞ		à	109 GVMGFPGP
ò	511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQ 558	q _Q	417 GVMGFPGP
ΩÞ	897 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLØ 956	ζō	169 GSPGFQGL
λ̈	559 GPGPAGPAGERGEQGPAGSPGFQGLPGPAGPGEAGKPGEQGVP 603	qq	477 GSPGFQGL
Д		ò	213
ò	604 GDLGAPGPSGPAG 616	qc	537 GANGAPGN
qq	1017 GPPGPPGPPG 1029	ò	259 GE
		q ₀	597 GKDGVRGL
RESULT US-10-1	3 04-889-8	ò	301 GPPGPPGA
; Seque ; Publi	; Sequence 8, Application US/10104889 ; Publication No. US20040086961A1	q	657 GADGQPGA
GEN	ERAL INFORMATION: APPLICANT: GRUSKIN, ELLIOT A.	λ ₀	342VGP
	BUECHTER, DOUGLAS BROKAW, JANE	đ	111 717 GAAGRVGP
	ZHANG, GUANGHUI PAOLELLA, DAVID	ò	394 GEOGVPGD
	TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES NUMBER OF SEQUENCES: 50	qa	 777 GADGPAGA
•	CORRESPONDENCE ADDRESS: ADDRESSER: DIMORTH & BARRESE	ò	454 GPAGP
	STREET: 333 EARLE OVINGTON BOULEVARD	ପ୍	837 GPMGPPGI
<u>,</u> .	STATE: OXICIOSEES STATES OCCUPATION. 11 C &	ò	511 GARGQAGV
	ZIP: 11553	;	
	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	2	
	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS	λõ	
	SOFTWARE: PatentIn Release #1.0, Version #1.30	qa	957 GPPGPPGS
	CURRENT AFFILCATION JAKE: AS A PELICATION NUMBER: US/10/104,889	λō	604 GDLGAPGE
	FILING DATE: 22-Mar-2002 CLASSIFICATION: <unknown></unknown>	QQ	1017 GPPGPPGF
	PRIOR APPLICATION DATA: APPLICATION NUMBER: US/09/169,768	1	,
•• •	FILING DATE: 09-OCT-1998	US-10-	-104-889-10
۰.	NAME: STEEN, JEFFREY S	, sed	; Sequence 10, Applica
	TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 228-8484		ENERAL INFORMATIC
			APPLICANT: GF
	INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:		iai
. •~ •	LENGTH: 1171 amino acids TYPE: amino acid		
	STRANDEDNESS: single		TITLE OF INVE
	TYPE: peptide		CORRESPONDENC
, US-10-1	; US-10-104-889-8		STREET: CITY: U
Query Best	Query Match 64.1%; Score 2237.5; DB 15; Length 1171; Best Local Similarity 60.2%; Pred. No. 2.1e-104; Most Local Similarity 60.2%; Mismarches 150; Indels 117; Gans 12;		STATE: N COUNTRY: ZIP: 113
Marci	ימרוזיל לוויים מוויים	. 	COMPUTER REAL

දුර අ <u>ගි</u>	1 G	GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 4	8 10
જે દ	49 0	GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 1 	108
3 &			168
a :	~ 0		212
경 임		 PGERGVQGPPGPAGPR	6
۸ŏ	213 -	TGLPGPPGERGPPGAPGAPGAPAGPKGPAGERGSPGPAGPKGSP 2	22
Db	537	GANGAPGNDGAKGDAGAPGAPGAPGGAPGERGAAGLPGPKGDRGDAGPKGADGSP	50
٥'n	259 (GEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGFPGPAGDGRP 3	300
Dp	597		929
, VO	301	GPPGPPGARGQ	₩ .
අධු	657		
Qy	342	VGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP	9
Dp QD	717 (77
λō	394 (GEGGVFGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP	45.
qq	777 (۵.	83
δλ	54	GPAGPKGS-PGEAGRPGEAGLPGAKGLTGS-PGS-PGPDGKTGPPGPAGQDGR-PGPPPP 5	51
QQ	837		מ
ολ	511 (AGAQ :	52
qq	897 (KGHRGFSGLQ	o, m
λŏ	559	GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEPGEPGCVP (9
Db	957 (pgspgepsgasgpagepgspgspgspgrdtpgrgprgprgprgpv	10
	604	LGAPGPSGPAG 616	
op qu	1017	GPPGPPGPPG 1029	
RESULT 4 US-10-104.; Sequence; Publicat GENERA	889- 8 10, tion	RESULT 4 US-10-104-889-10 IS-20-10-10, Application US/10104889 Publication No. US20040086961A1 GENERAL INFORMATION:	
	APPLI	FANT: GRUSKIN, ELLIOT A. BUECHTER, DOUGLAS BROKAW, JANE	
	TITLE	LE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES BEBR OF SEQUENCES: 50	
	CORRE	SPENDENCE ADIMOSTI. ADDRESSES: DILWORTH & BARRESE TYPEET: 333 BARLE OVINGTON BOULEVARD	
		IITY: UNIONDALE STATE: NY	
		COUNTRY: U.S.A. ZIP: 11553	
	COMPU	TER READABLE FORM:	

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RESULT 5
US-10-216-705-21
Sequence 21, Application US/10216705
Publication No. USZ0030056973A1
Sequence 21, Application US/10216705
Publication No. USZ0030056973A1
APPLICANT: Waristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Me
TITLE OF INVENTION: Obtaining Such and Their Uses
TITLE OF INVENTION: Obtaining Such and Their Uses
TILE OF INVENTION: US 002-08-09
CURRENT APPLICATION NUMBER: US/10/216,705
CURRENT APPLICATION NUMBER: US 09/331,347
PRIOR APPLICATION NUMBER: US 09/331,347
PRIOR APPLICATION NUMBER: US 09/331,347
SEQ ID NO 21
SEQ ID NO 21
SEQ ID NO 21
SEQ ID NO 21
LENGTH: 1464
TYPE: PRT
ORGANISM: Home sapiens
US-10-216-705-21
                                                                                                         ||||||
957 GPPGPPGSPGGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRIGDAGPV 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 GANGAPGUDGAKGDAGAPGAPGAPGAPGAPGLQGAPGERGAAGLPGPKGDKGDAGPKGADGSP 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                638 GSPGFPQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGSPGRGGPGGAGGDGRPGPPGPPGARGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     878 GAAGRVGPPGPSGNAGPPGPPGPPGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.1%; Score 2237.5; DB 14; Length 1464; larity 60.2%; Pred. No. 2.4e-104; Conservative 23; Mismatches 152; Indels 117; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------
                                                                                                                                                                                                  .017 GPPGPPGPPGPPG 1029
                                                                                                                                                              604 GDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                559 GPPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Simi
Matches 441;
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Best Local Similarity 60.2%; Pred. No. 2.3e-104;
Matches 441; Conservative 23; Mismatches 152; Indels 117; Gaps
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, USFREY S
TELEPHONE: (516) 228-8816
TELEPHONE: (516) 228-8816
TELEPHONE: (516) 228-8816

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids

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) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-104-889-10
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Db 998 GPMGPPGLAGPPGESGREGAPGAPGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 1057 Qy 511 GARQQACWGFPGPKGAAGERGVPGPAGACGDAGKDGEAGAQ 558 Db 1058 GPAGKSGDRGETGPAGPAGARGPAGPGGPRGDKGTKGHRGFSGLQ 1117 Qy 559 GPPGPAGPAGERGEGGPAGSPGFQGLPGPAGPRGEGGVP 603	1, Application US/10357851 1, Application US/10357851 1on No. US20040151731A1 INFORMATION: NT. Jicha, Douglas L. FINUENTION: T-Lymphocyte Reactivity with Colling INVENTION: Abdominal Acrtic Aneurysm Patient FERENCE: 13376US - APPLICATION NUMBER: US/10/357,851 - FILMO DATE: 2003-02-04 FILMO DATE: 2003-02-04 FILMO SAPIENCE SAPIENCE SM: Homo Sapiens	Query Match 64.1%; Score 2237.5; DB 16; Length 1464; Best Local Similarity 60.2%; Pred. No. 2.4e-104; 104. Matches 441; Conservative 23; Mismatches 152; Indels 117; Gaps 12; Qy 1 1 QPP	4-4 4-	DD 578 GWGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGBAGAQGPPGPAGPRGEGGPA 637 QY 169 GSPGFQGLPGPAGPPGBAGKPGBCGVPGDLGAPGPSGPAGEPGP 212		GVRGLTGPPGABAGESGPSGPSGPSGPSGPSGPSGPSGPSGPSGPSGPSGPSGPS	3.42 8.78 8.78 8.44

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938 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGERGPP 997
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           GVMGFPGPKGAAGEPGKAGERGVPGPPGA---- 341
                                                                                                               342 -----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                      GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
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                                                      818 GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP
                                                                                                                                                                878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
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62.0%; Pred. No. 3.6e-104;
ive 21; Mismatches 154;
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Best Local Similarity 62.0%
Matches 438; Conservative
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; ORGANISM: Sus scrofa
US-10-402-089-8
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US-10-402-089-8
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Publication No. US20040191819A1
GENERAL INFORMATION:
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Buyer Pharmaceuticals Corporation
APPLICANT: Bigwood, Douglas
TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
FILE REFERENCE: 515
CURRENT APPLICATION NUMBER: US/10/788,792
CURRENT APPLICATION NUMBER: US 60/450,655
PRIOR APPLICATION NUMBER: US 60/450,655
NUMBER OF SEQ ID NOS: 254
SOFTWARE: Patentin version 3.2
SEQ ID NO: 254
                                                                                                                                                                                            1118 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGXDGLNGLPGPIGPPGPRGRTGDAGPV 1177
                                                                                                                                                                                                                                                                                                                        1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLØ 1117
                                                                                                                                                             GPAGP----KGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                                                                                                                                                                                                                                                                                                                                                                                 GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGEPGEAGKPGEQGVP 603
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GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937
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                                                                                        511 GARGQAGVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
                                                      GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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; ORGANISM: Homo sapiens
US-10-788-792-150
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13; 180 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120 591 GPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAK 711 213 --TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE------A 261 532 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP 94; Gaps

us-10-658-989a-2.rapb

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952 RGERGFPGLPGPSGEPGKQGPSGPSGPRGPPGPMGP---PGLAGPPGESGREGAPGAEGS 1008
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                                                                                                     GRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGP---PGPPGARGQAGVMGF- 317
                                                                                                                          ---RGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGP 422
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                                                        318 --- PGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPPGPAGPAGE
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652 GPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAK
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                                   213 --TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-
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Publication No. US20040157329A1

GENERAL INFORMATION:
APPLICANT: APPLICANT: The University of Sydney
TITLE OF INVENTION: Matrix gene expression in cho;
FILE REFERENCE: 500311

CURRENT APPLICATION NUMBER: US/10/468,091:
CURRENT PILING DATE: 2003-08-13

PRIOR APPLICATION NUMBER: AU PR3116

PRIOR FILING DATE: 2011-02-15

NUMBER OF SEQ ID NOS: 42

SOSTWARE PATENTING DATE: PATENTING DATE: PROCE PROCE
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ORGANISM: Homo sapiens
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                                                                                                                            ---PGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAOGPPGPAGE
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Sequence 8, Application US/10402072A
Publication No. US20040018592A1
GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Neff, Thomas B.
APPLICANT: Seeley, Todd W.
APPLICANT: Seeley, Todd W.
TITLE OF INVENTION: BOVINE COLLAGENS AND GELATINS
FILE REFERENCE: FP0402.2 CON
CURRENT APPLICATION UNMBER: US/10/402,072A
CURRENT FILING DATE: 2003-03-66
PRIOR APPLICATION NUMBER: US 09/709,700
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH. 14.40
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Pred. No. 3.6e-104;
1; Mismatches 154;
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Best Local Similarity 62.0%;
Matches 438; Conservative 2:
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US-10-402-072A-8
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TYPE: PRT
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    158 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 517
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                                                                                                                                                                                                                          GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                 18 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                      698 GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
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Sequence 16, Application US/10104889

Sequence 16, Application US/10104889

Publication No. US20040086961A1

GENERAL INFORMATION:
BUEGHTER, DOUGLAS
BUEGHTER, DOUGLAS

HANG, GUANGHUI
PAOLELLA, DAVID

TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----
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STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
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COMPUTER: IBM PC compatible
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COMPUTER READABLE FORM:
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GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDKGDAGPKGADGSP 754
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                                                                                                                                                                                                                   301 GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
                                                                                                                                                                                                                                                                                                ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
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                                                            --TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   511 GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE
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APPLICANT: Hyseq, inc.
APPLICANT: Tang et al
TILE OF INVENTION: NO.
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-37
PRIOR FILING DATE: 2000-01-37
PRIOR FILING DATE: 2000-01-37
PRIOR FILING DATE: 2000-03
PRIOR FILING DATE: 2000-03
PRIOR FILING DATE: 2000-03
PRIOR FILING DATE: 2000-09-15
NUMBER: OF SEQ ID NOS: 944
SECTIVANE: FASICERQ FOR WINDOWS VERSION 3.0
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Publication No. US20030232054A1
GENERAL INFORMATION:
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US-10-291-265-243
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US-10-291-265-243
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Best Local S:
Matches 440
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                                                                                                                                RESULT 14
US-10-058-124-18
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-104-889-16
                                                                                                                                                                NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                                                                                   FELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
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Best Local Similarity 60.0%
Matches 440; Conservative
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Carrying Out to the Presence of
49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
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                                                                                                                                                                                                                            Sequence 18, Application US/10058124
Publication No. US20030119058A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Qvist, Per
Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
method and Use of the Method to Diagnose
Disorders Associated with the Metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1341;
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63.9%; Score 2228.5; DB 14
Best Local Similarity 60.0%; Pred. No. 6.4e-104;
Matches 440; Conservative 23; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFRAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve-
CURRENT APPLICATION NUMBER: US/10/058,124
FILING DATE: 29-Jan-2002
CLASSIFICATION: <unh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/570,573
FILING DATE: 2002-MAY-12
APPLICATION NUMBER: 08/187,319
FILING DATE: 
vUnknown>

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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Я
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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SEQUENCE CHARACTERISTICS:
                                                                                                                 1029
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                                                                                                                                                                                                                                                                                                                       GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
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              -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
                                                                                                      574 GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
                                                                                                                                    GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP
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                                                                                                                                                                                  ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 261, Application US/0918715

Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Brad & C. Croix

APPLICANT: Bert Vogelstein

APPLICANT: Renneth Kinzler

TILE REFERENCE: 1107.00134

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/22,599

PRIOR PLICATION NUMBER: 60/224,360

PRIOR PLICATION NUMBER: 60/224,360

PRIOR PLING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR PLING DATE: 2000-08-01

PRIOR PLING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 358

SOFTHARE: PSESSEQ for Windows Version 3.0

SEQ ID NO 261

LENGTH: 1464
                                            GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-
                                                                                                                                                                                301 GPPGPPGARGQ-----
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US-09-918-715-261
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US-09-918-715-261
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                                                                                                458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                        GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                               213 -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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                                                          GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                       Gaps
                       117;
                  Indels
                                                                                                                                                                                                                                                                                               GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-
il Similarity 59.9%; Pred. No. 7.7e-104; 439; Conservative 23; Mismatches 154;
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Job time : 84.3776 secs
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  Best Local
Matches 43
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63.9%; Score 2227.5; DB 10; Length 1464;

Query Match

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 18, 2004, 13:31:10 ; Search time 24.4569 Seconds (without alignments) 2427.363 Million cell updates/sec Run on:

US-10-658-989A-2 3488 1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 617 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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type VII collagen	collagen alpha 1(X	collagen alpha 4(I	collagen alpha 2(I	collagen alpha 2(I	collagen alpha 1(I	collagen alpha 1(V	collagen alpha 1(X	collagen alpha 1(I	collagen alpha 3(I	collagen alpha 2(I	collagen COLF1 - f	collagen alpha 2(I	hypothetical prote	collagen alpha 1(X	collagen alpha 3(I
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1556.5															
30	31	32	33	34	35	36	37	38	9	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 CCHUIS
	collagen alpha 1(I) chain precursor - human NyAlternate names: procollagen alpha 1(I) chain
	C;Species: Homo sapiens (man) C;Date: 12-Aug-1981 #sequence revision 04-Oct-1996 #text change 09-Jul-2004 C;Accession: 160114; S01143; Ā93335; 155254; A39943; 155237; A35233; S09400; B90567; S1:
	5269; A29439; I53466; A02852; I37247 R.P.Alessic, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
	Gene 6/, 105-115, 1988 A.Title: Complete nucleotide sequence of the region encompassing the first twenty-five A.Reference number: 160114; MUID:88329734; PMID:2843432
	A;Accession: I60114 A;Status: translated from GB/EMBL/DDBJ
	A,Molecule type: DNA A,Residues: 1-369,'L',371-589 <dal></dal>
	A; Cross-references: UNIPROT: P02452, UNIPROT: Q14992, UNIPROT: Q16053; UNIPROT: Q13896; UNI R: Tromp. G.: Knivaniemi. H.; Stacev, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Proc
	Biochem J. 253, 919-922, 1988 A. Title. Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human
	A; Reference number: S01143; MUID: 89025644; PMID: 3178743
	A; Accession: Solida A: Molegule tyme: mRNA
	A; Residues: 1-472 <tro></tro>
	R;Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.
	Nature 310, 337-346, 1984
	A; Reference number: A93335; WUID: 84270697; PMID: 6462220
	Astocession: A9335
	A;Residues: 1-58, V., 60-181 <chu></chu>
	A; Cross-references: EMBL:X00820; NID:g35657; FIDN:CAA255941; FIDS:g35657; As wet w
	di meri namitati rii de neci
	A; Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene en
	A; Accession: ISS254
	A;Status: translation not shown; translated from GB/EMBL/DDBJ
	A, Molecule type: DNA
	PID:91803
	R. Bornstein, P.; McKay, J.; Moriahima, J.K.; Devarayalu, S.; Gelinas, R.E.
	A; Title: Regulatory elements in the first intron contribute to transcriptional control
	A;Reference number: A39943; MUID:88097389; PMID:3480516 A:Accession: A39943
	A; Molecule type: DNA
	A.Kesiduse: 1-44 cMCA. A.Cross.references: GB:003559; NID:g180876; PIDN:AAA52052.1; PID:g553238
_	R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

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A; Reference number: A35336; MUID:90252792; PMID:2339700
A; Accession: A35336
A; Accession: A35336
A; Accession: A35336
A; Accession: A35336
A; Accession: B; 722-737, E', 739-745 < WAL>
A; Residues: 710-720, E', 722-737, E', 739-745 < WAL>
A; Residues: 710-720, E', 722-131
A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R; Forlino, A, 2012-2206, 1994
A; Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the c, A; Reference number: 154365, MUID:95187161; PMID:7881420
A; Accession: 154365
A; Scatus: translated from GB/EMBL/DDBJ
A; Residues: 746-766, S', 768-781, FOR>
A; Residues: 746-766, S', 768-781, FOR>
A; Residues: 76-766, S', 768-781, FOR>
A; Residues: 750-1; Wallis, GA.; Byers, P.H.
C; Biol. Chem. 268, 18218-18225, 1993
A; Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty A; Reference number: A47426; MUID:93352646; PMID:8349697
                                                                                                                A; Molecule type: mRNA
A; Residues: 342-352, (C', 354-359 < WIZ>
A; Residues: 342-352, (C', 354-359 < WIZ>
A; Residues: 342-352, (C', 354-359 < WIZ>
A; Cross-rences: GB: S64717; NID: 9408195; PIDN: AAB27677.1; PID: 9408196
A; Note: mutant sequence from patient with osteogenesis imperfects
B; Bernard, M.P.; Chu, M.J.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
Biochemistry 22, 5213-523, 1981
A; Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal A; Reference number: A90476; MUID: 84080385; PMID: 6689127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Biol. Chem. 260, 691-694, 1985
. Yittle: Multiexon deletion in an osteogenesis imperfecta variant with increased type II
. Reference number: A22161; MUID:85104934; PMID:2981843
. Accession: A22161
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AjResidues: 472-594, R',586-607 cCH3>
AjResidues: 472-594, R',586-607 cCH3>
AjCross-references: GB:K03178; GB:K03179; NID:g179612; NID:g179613; PIDN:AAA51847.1; PID
AjNote: the authors translated the codon CGT for residue 595 as Pro
R;Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
AjTitle: Variable expression of osteogenesis imperfecta in a nuclear family is explained
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A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: GB:S64596; NID:g407589; PIDN:AAB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different mut
A;Accession: B47426
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R; Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Ni
J. Biol. Chem. 263, 14605-14607, 1988
A;Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide
A;Reference number: 155269; WUID:89008319; PMID:3170557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A90476
;Molecule type: mRNA;
;Residues: 425-1250, 'X',1252-1328,'S',1330-1390,'X',1392-1464 <BER>;Cross-references: 481-1250, 'X',1252-1328,'S',1330-1390,'X',1392-1464 <BER>;Cross-references: 481-1250, NID: 9180391; PIDN:AAA51995.1; PID: 9180392; NOte: sequence partially completed for missing nucleotides by A29439; Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
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;Residues: 1179-1387,'R',1389-1464 <CH7>
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Experimental source: fetal cell 86-237
Accession: D47426
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Residues: 1179-1336,1339-1464 <CH6>
Experimental source: fetal cell 86-146
                                                                                   Status: translated from GB/EMBL/DDBJ
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Residues: 1179-1464 <CH4>
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A. Title: The estructural analysis of the human pro-alpha 1 (1) collagen gene. Promoter a A./Reterence number: 155277 (WID:5310970), PWID:2857713 (I) 1995
A./Stetus: translation not shown; translated from GB/BMBL/DB3J
A./Accession A./Stassion and A. Vitro and A. Vit
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A; Cross-references: GB:S67495; NID:9239007; FIDN:AAB20350.1; FID:9239008
A;Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
J. Biol. Chem. 245, 5042-5048, 1970
A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
A; Reference number: A92069; MUID:71001508; PMID:4319110
A;Recession: A92069; MUID:71001508; PMID:4319110
A;Recession: A92069; MUID:71001508; PMID:4319110
A;Recession: A92069; MUID:71001508; PMID:4319110
A;Residues: 263-268 cMOR>
A;Residues: 263-268 cMOR>
A;Residues: 263-268 cMOR>
A;Reference number: S15989; MUID:90326017; PMID:2374517
A;Residues: 281-300, 1990
A;Title: Segmental amplification of the entire helical and telopeptide regions of the cIC
A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 cLAB>
A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 cLAB>
A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 cLAB>
A;Reference number: ISS905; MUID:93339042; PMID:8339541
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A, Residues: 258-268;1347-1357 < DEA>
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Query Match
Best Local Similarity
Matches 432; Conserv
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C;Species: Mus musculus (house mouse)
C;Daceies: Jan-1995 #sequence revision 25-Apr-1997 #text change 09-Jul-2004
C;Accession: S51243; S16374; Z5382; I49559; I49557; S39789; I48300; S21626
R;Li, S.W.; Khillan, J.; Prockop, D.J.
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               A.Molecule type: DNA
A.Residues: 1187-1194, C', 1196-1220 CCOH>
A.Kresidues: 1187-1194, C', 1196-1220 CCOH>
A.Kresidues: 1187-1194, C', 1196-1221
A.Note: mutant sequence from a patient with mild osteogenesis imperfecta
A.Mackelae, J.K.; Raassina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A.Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptic
                                                                                                                                           Query Match 63.9%; Score 2228.5; DB 1; Length 1464; Best Local Similarity 60.0%; Pred. No. 4.2e-105; Matches 440; Conservative 23; Mismatches 153; Indels 117;
from GB/EMBL/DDBJ
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Matria Biol. 14, 323-59, 1934 asquence for the mouse pro-alpha-1(I) chain of type I Assestance The Mouse to Complete cDNA coding sequence for the mouse pro-alpha-1(I) chain of type I Assestance The Complete CDNA 
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Ajdene: COLIAI
Collagen alpha 1(1) chain, fibrillar collagen carboxyl-terminal homology
Cjsuperfamily: collagen alpha 1(1) chain, fibrillar collagen carboxyl-terminal homology
Fig. 1-22/Domain: signal sequence #status predicted <SIG>
Fig. 1-22/Domain: amino-terminal propeptide #status predicted <PRO>
Fig. 0-89/Domain: von Willabrand factor type C repeat homology <VWC>
Fig. 1-453/Product: collagen alpha 1(1) chain #status predicted <WAT>
Fig. 24-1453/Pomain: fibrillar collagen carboxyl-terminal homology <FCC>
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A;Residues: 1-80,'E',82-105,'D',107-147 <REF>
A;Cross-references: EMBL:X54876; NID:950486; PIDN:CAA38657.1; PID:950487
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llarity 58.9%; Pred. No. 6e-104;
Conservative 22; Mismatches 162; I
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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11;

Gaps

Indels

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collagen alpha 1(I) chain - rat (tentative sequence) (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
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                                                                                                    GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPAGPPGARGQA
                                                                                                                                                                             687 GNNGAPGNDGAKGDTGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDAGPKGAPGSP
-GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                 GPPGPAGEEGKRGARGEPGPSGLPGPPGERGGPGSRGFPGADGVAGPKGPSGERGAPGPA
                                                                                                                                                      GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                 ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
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                                                                         GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
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A; Molecule type: protein
A; Residues: 1037-1042 < EERs.
A; Residues: 1037-1042 < EERs.
A; Residues: 1037-1042 above correspond to the carboxyl end of the protein
A; Note: residues 1037-1042 above correspond to the crippepide repeating unit (c) Comment: Most of the prolines at the third position of the trippepide repeating unit (c) Comment: Most of the prolines at the third position of the trippepide repeating unit (c) Comment: Pro-1002 is the only 3-hydroxyproline and the only hydroxylated propertion in pc c; Superfamily: collagen alpha 1(1) Chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer; F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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GPPGPPGAPGEQGPSGASGPAGPRGPPGSAGAAGKDGLNGLPGPIGPPGPRGRTGEVGPV 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 1042;
                                                                                                                                                                                                                                                                                                                                                                                            Score 2151.5; DB 1; Length
Pred. No. 2.4e-101;
7; Mismatches 175; Indels
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Matches 424; Conserv
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A.Residues: 419-567 <BU3>
A.Residues: 419-567 <BU3>
A.Residues: 419-567 <BU3>
A.Residues: 419-567 <BU3>
A.Residues: 8tin
B.S. 204 1973
B.S. 204 1973
A.Title: Structural and immunogenic properties of a major antigenic determinant in neut
A.Title: Structural and immunogenic properties of a major antigenic determinant in neut
A.Residues: 582-294 1973
A.Accession: A31209
A.Accession: A31209
A.Accession: A31209
A.Accession: A19120
A.Accession: A19130
A.Accession: A19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AGSPGFQGLPGPAGPPGEAGKPGEQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 GEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQGPSGAPGPK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVPGDLGAP-------GPSGPA-----GBPGPTGLPGPPGERGGP 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 GPKGSPGEAGRPGE-----AGLPGAKGLT-----GSPGSPGPD---GKTGPPGPAGQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 GRPGPPGPPGARGQAGVMGFPGPKGAAGE-----PGKAGERGVPGPPGAVGPAGKDGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 GPPGAPGPGGPGBPGBPGASGPMGPRGPPGFWGDPGFWGDDGBAGKPGRPGPPGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 GARGLPGTAGLPGWKGHRGFSGLDGAKGNTGPAGPKGEPGSPGENGAPGQMGPRGLPGER
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59.5%; Pred. No. 1.8e-94;
tive 28; Mismatches 119; Indels 123;
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Best Local Similarity 59.59
Matches 396; Conservative
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; Molecule type: protein
; Molecule type: protein
; Molecules: 140-238 cBt)
; Residues: 140-238 cBt)
; Baperimental source: skin
; Balian, G.; Click, E.M.; Hermodson, M.A.; Bornstein, P.
iochemistry 11, 3798-33806, 13380, 133806, 133805, 1341619: Structure of rat skin collagen alphal-CB8. Amino acid sequence of the hydroxyla
; Attle: Structure of sat skin collagen alphal-CB8. Amino acid sequence of the hydroxyla
; Reference number: A90362; MUID:73006942; PMID:4342027
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Biochemistry 8, 63-71, 1969
A,Title: Comparative sequence studies of rat skin and tendon collagen. II. The absence c A,Reference number: A90559, MUID:69155173; PMID:5777344
A,Contents: CNBYO and CNBr1
A,Accession: A90559
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A; Residues: 239-418 e Balz>
A; Residues: 239-418 e Balz>
B; Residues: 239-418 e Balz>
B; Residues: 239-418 e Balz>
B; Butler, W.T.; Underwood, S.P.; Finch Jr., J.E.
Biochemistry 13, 294-6-2953, 1974
A; Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino A; Reference number: A90379; MUID: 74271984; PMID: 4366532
A; Accession: A90379
A; Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of rat skin
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A; Residues: 1-19 <BO1>
A; Residues: 1-19 <BO1>
A; Residues: 1-19 <BO1>
A; Residues: 1-19 <BO1>
A; Note: 19 <BO1
A; Note: sequences from skin and tendon appear to be identical
A; Note: the amino-terminal tetrapoptide may be removed by limited proteolysis during shikang, A.H.; Bornstein, P.; Piez, K.A.
Biochemistry 6, 788-795, 1967
A; Title: The amino acid sequence of peptides from the cross-linking region of rat skil
A; Reference number: A90552; MUID:67162268; PMID:5337886
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A;Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. The
A;Reference number: A90566; MUID:70085124; PMID:5411206
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Tittle: The incomplete hydroxylation of individual prolyl residues in collagen.
Reference number: A92029; WUID:67165368; PMID:4290711
CONTENTS: CNBT2.
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Molecule type: protein;Residues: 56-102 <BU1>
Experimental source: skin
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Molecule type: protein
Residues: 5-19 <KAN>
Experimental source: skin
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R,Bornstein, P.
J. Biol. Chem. 2
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8 6 8 6 8 8		6 8 6 8 6	448 GERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD 489
RESULT T45467 C011467 C) Speci C) Access R) Richa R) Refer A) Access A) Access A) Access A) Access A) Access A) Access A) Access A) Cross	RESULT 5 collagen alpha 1(II) chain precursor [imported] - horse N;Alternate names: type II collagen N;Alternate names: type II collagen C;Species: Equus caballus (domestic horse) C;Species: Equus caballus (domestic horse) C;Accession: T45467 R;Richardson, D.W.; Dodge, G.R. R;Richardson, D.W.; Dodge, G.R. submitted to the EMBL Data Library, June 1996 A;Reference number: Z22977 A;Accession: T45467 A;Accession: T45467 A;Accession: T45467 A;Accession: T45467 A;Residues: 1-1418 - RIC> A;Residues: 1-1418 - RIC> A;Residues: 1-1418 - RIC> A;Cross-references: UNIPPOT:Q28396; EMBL;U62528; PIDN:AAB05773.1 C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;	1.11	### ### ##############################
Query Best I Matché Qy Db	4, DB 2; Length 1418; ches 189; Indels 138; Gaps 14; ches 189; Indels 138; Gaps 14; DGVAGPKGPAGERGSPGPAGPKGSPGBAGRP 60 DGAGKPGKSGERGPPGGARGFPGTPGLP 215	A,Residue A,Cross-r R,Su, M.W Nucleic A,Nitle: 1 A,Title: 1 A,Referent A,Modecsid	s: 1-103 <rya> - Lae, B.; Ramirez, F.; Machado, M.; Horton, W Lae, B.; Ramirez, F.; Machado, M.; Horton, W Cids Res. 17, 9473, 1989 - Nucleotide sequence of the full length cDNA encoding for human type II procolla - on number: S06715; MUID:90067946; PMID:2587267 - Experimental Control of the full length cDNA encoding for human type II procolla - on: S06715 - or NUMBER: S06715; MUID:90067946; PMID:2587267</rya>
oy oy ob	90 27 13	A, Residue A, Cross-r. A, Note:a A, Notes:a B, Othem. A, Referen A, Referen A, Referen A, Recession	s: 1-28, 'R', 99-1487 <su2> deferences: BRBL:XX54688, NID:g29515, PIDN:CAA34488.1; PID:g29516 lternative splice form 1 lternative splice form 1 'M.; Metsaeranta, M.; Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L. Jr. 285, 287-294, 1992 Structural analysis of the regulatory elements of the type-II procollagen gene. ce number: S24270; MuID:92344585; PMID:1637314</su2>
& & & & & & & & & & & & & & & & & & &	GAAGNPGTDGAKGGBAGGPPGFAGPAGERGEGGPAGSPGFOGLP GAAGNPGTDG1PGAKGSAGAPG1PGPRGPRGPPGPPGPGPGTGEPG1AGFK GPAGPPGEAGKPGEGGVPGDLGAPGPPGPPGPPGPPGPTGLPGPLGPKGQTGEPG1AGFK GPAGPPGEAGKPGEGGVPGDLGAPGPSGPAGEPCPTGLPGPPGERGGPGSRGFPGADGVA	A Actatus: A Molecul: A Residue: A A Cross-rr A Note: U R Numez, U Gene 44, A TREFERE	Taristation not shown e type: DNA s: 1-28 <vik> s: 1-28 <vik> s: 1-28 <vik> https://documerry.com/ https://docum</vik></vik></vik>
8 6 8 6 8 6 8 6	238 GPKCPAGERGSPGPAGPKGSPGEAGLPGSPGSPGSPGSPGSPGSPGSPGSPGSPGSPGSPGSPGSP	A,Accessin A,Rolecul A,Ross-rr A,Cross-rr Blochem . A,Title: 6 A,Accessic A,Accessic A,Accessic A,Rosidue A,Rosidue A,Rosidue A,Rosidue A,Rosidue	A,Accession: A24828 A,Accession: A24828 A,Molecule type: DNA A,Residues: 1-8, T', 10-28 <nun> A,Cross-references: GB:MZ5698; NID:g180872; PIDN:AAA52051.1; PID:g553237 A,Cross-references: GB:MZ5698; NID:g180872; PIDN:AAA52051.1; PID:g553237 R,Baldwin, C.T.; Reginato, A.M.; Smith, C.; Jimenez, S.A.; Prockop, D.J. B,Accession: C. 262, 521-528, 1989 A,Title: Structure of cDNA clones coding for human type II procollagen. The alpha-1(II) A,Reference numbers: S06496, MUID:90026318; PMID:2803268 A,Accession: S06496 A,Accession: S06496 A,Accession: SNEL:XI6711; NID:g30040; PIDN:CAA34683.1; PID:g30041 A,Cross-references: BMBL:XI6711; NID:g30040; PIDN:CAA34683.1; PID:g30041 A,Note: alternative splice form 1 R;Ryan, M.C.; Sandell, L.J. J. Biol. Chem. 265, 10334-10339, 1990</nun>

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A; Note: mutant sequence associated with perinatal lethal hypochondrogenesis
R; Tiller, G.E.; Rimoin, D.L.; Murray, L.W.; Cohn, D.H.
Pyco. Natl. Acad. Sci. U.S.A. 87, 389-3893, 1995
A; Titler Tandem duplication with a type II collagen gene (COLZAI) exon in an individual particle transport of the state o
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A; Accession: A24561
A; Molecule type: DNA
A; Mesiduces: 1256-1358 «NUN2>
A; Mesiduces: 1256-1358 «NUN2>
A; Cross references: 1268-M12048; NID:9180017
A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: this cranslation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: the codons given for 133-Lys (AGG) and 1350-Gly (GCA) are inconsistent with th R; Sandrez A; Toolation and partial characterization of the entire human pro alpha 1(II) col A; Accession: 859491
A; Mesiduces: 7-28, RX, 99-114;541-578;786-802;1055-1056, N', 1058-1068, T', 1070-1109;1200-A; Accession: 184453
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residuces: T-28, ANDAS
A; Residuces: 7-28, ANDAS
A; Molecule type: DNA
A; Molecule type
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal pro
R; Strom, C.M.; Upholt, W.B.
Mucleic Acide Res. 12, 1025-1038, 1984
A; Title: Isolation and characterization of genomic clones corresponding to the human ty
A; Reference number: A21733; MUID: 84118798; PMID: 6320112
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A;Residues: 1245-1295 SSTR1>
A;Accession: B21733
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 894-909, PEX SSTR2>
A;Cross-references: GB:K01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
A;Cross-references: GB:K01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
A;Nunez, A,M., Francomano, C:, Young, M.F.; Martin, G.R.; Yamada, Y.
Biochemistry 24, 6343-6348, 1985
A;Title: Isolation and partial characterization of genomic clones coding for a human pr
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A,Status: translated from GB/EMBL/DDBJ
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                                  Title: Differential expression of a cysteine-rich domain in the amino-terminal propept
Reference number: A35428; MUID:90285153; PMID:2355003
Accession: A35428
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A;Reference number: 805000; MUD:89325561; PMID:2753125

A;Accession: 805000; MUD:89325561; PMID:2753125

A;Accession: 805000; MUD:89325561; PMID:2753125

A;Residues: 630-640, 'A', 642-785 «VIK2>

A;Residues: 630-640, 'A', 642-785 «VIK2>

A;Cross-references: EMB:13658; NID:923951; PIDN:CAA34278.1; PID:g1335018; PIDN:CAA3427

P;Bogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D.J. Biol. Chem. 267, 22522-22526, 1992

A;Reference number: A44309; MUID:9305448; PMID:4429602
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J. Biol. Chem. 267, 22522-22526, 1992

A.Title: An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain pro A; Reference number: A44309; WUID:33054484; PMID:1429602

A; Accession: A44309

A; Accession: A44309

A; Statuus: nucleid acid sequence not shown; not compared with conceptual translation

A; Residues: 752-831, 'PA', 834,'F', 836-1005,'K', 1007-1036,'Q', 1038-1052,'E', 1054-1068,'T', A; Cross-references: GB:L00977, NID:GB:R012, PIDN:AAB23944.1; PID:G228774

A; Note: sequence extracted from NCBI backbone (NCBIP:117273); parts of this sequence wer A; Note: this translation is not annotated and this publication is not cited in GenBank e
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A; Residues: 171-172, 'C', 174-175 < ALA>
A; Note: mutant sequence from a family with family with primary generalized osteoarthriti
K; Diab, N; W; V; J; J; Byre, D.R.
Biochem. J; 314, 327-332, 1996
A; Title: Collagen type IX from human cartilage: a structural profile of intermolecular c
A; Reference number: $64673; MUID: 96195147; PMID: 8660302
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A. Molecule type: protein
A. Meskidues: 188-149, /X. / 1912-195,1224-1230, /X. / 1232-1236 cDIA>
A. R. Franc, S.; Marzin, B.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage, Bur. J. Biochem. 234; 125-131, 1995
A. Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil cax A. Reference number: 863514; MUID:96096730; PMID:8529631
A. Accession: 863514
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A/Notcession: A30147
A/Notcession: A30147
A/Notcession: A30147
A/Residues: 104-157/P/,159-236 <SUM>
A/Residues: 104-157/P/,P/,159-236 <SUM>
A/Cross-references: GB:J03065; GB:M23660; GB:M25656; GB:M25730; GB:M32168;
A/Cross-references: GB:J03065; GB:M23660; GB:M25656; GB:M25730; GB:M32168;
A/Cross-references: GB:J03065; GB:M25660; GB:M25660; D.J.
Brocc. Natl. Acad. Sci. U.S.A. 87, 6565-6569; 1990
A/Title: Single base mutation in the type II procollagen gene (COL2A1) as a cause of paycession: A33116
A/Roccession: A33116
A/Roccession: A33116
A/Roccession: A33116
                                  A;Title: Differential expression of a cysteine-rich domain in the amino-termin A;Reference number: A35428; MUD: 90285153; PMID: 2355003
A;Accession: A35428
A;Accession: A35428
A;Accession: A35428
A;Molecule type: mRNA
A;Residues: 27-81, '1.', 83-103 < RYA2>
A;Note: alternative splice form 2; splicing appears to be under developmental R;Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F.
Genomics 4, 438-441, 1989
A;Title: Organization of the exons coding for Pro alpha-1(II) collagen N-prope A;Reference number: A30147; MUD: 89233138; PMID: 2714801
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A; Residues: 243-261;575-590;756-763,'X',765-779 <FRA>
R; Tiller, G. E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, Am. J. Hum. Genet. 56, 388-395, 1395
A; Title: An RNA-splicing mutation (G+SIV320) in the type II colla A; Reference number: I38867; MUD: 95150028; PMID: 7847372
A; Accession: I38867
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A.Molecule type: DNA
A.Residues: 1-1419 (ART>
A.Molecule Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilag
A.Accession: A44885, MUID:91347939; PMID:1879363
A.Accession: A44885
A.Accession: A4885
A.Accession:
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            preliminary; not compared with conceptual translation
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A;Molecule type: DNA
A;Residues: 541-560 <SAN3>
A;Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A;Accession: 137251
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collagen alpha 1(II) chain precursor - mouse
collagens alpha 1(II) chain precursor - mouse
collagens: Mus musculus (house mouse)
c)species: Mus-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999
C)Accession: A41182; A4488
R)Accession: A41182, A4488, 1991
J. Biol. Cham. 266, 18862-18889, 1991
A)File: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, A)File: Mouser: A1182; MUID:91358489; PMID:1885613
                                                                                                                                                                                                                                                                                                                                                     344
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; Pred. No. 8.5e-91;
34; Mismatches 189; Indels 138;
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CONTRICT TO CONTRICT CANDING (TENTATIVE SEQUENCE) (fragments)
CONTRIGHED 1(1) Chain - bovine (tentative sequence) (fragments)
CONTRICT CACCOSTOR AND 157, AN
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A,Residues: 75-779 <RA2>
A,Experimental source: 8kin
C,Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydro
C,Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are
                                            978
                      GLOGPAGAPGEKGEPGDDGPSGLDGPPGPQGLAG
GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                         945
  583
    8 8
                                                          Collagen alpha 1(II) chain precursor (long splice form) - mouse
C.Species: Mss musculus (house mouse)
C.Species: Mss musculus (house mouse)
C.Species: Mss musculus (house mouse)
C.Accession: B41182
M. Hetsacranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
V. Biol. Chem. 266, 16862-16869, 1991. Complete nucleotide sequence, exon structure, and A; Teference number: A41182; MUD:91358489; PMID:1885613
A; Reference number: A41182; MUD:91358489; PMID:1885613
A; Recession: B41182
A; Cocession: B41182
A; Cocession: Miles in the compared with conceptual translation
A; Residues: 1-1487 Amer.
A; Coss-references: UNIPROT:062031; UNIPROT:062033; GB:M65161
C; Cinperfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime F; 32-91/Pomain: von Willebrand factor type C repeat homology <PKC>
F; 1259-1487/Domain: fibrillar collagen carboxyl-terminal homology <PKC>
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Best Local Similarity 51.9%; Pred. No. 3e-90;
Matches 391; Conservative 36; Mismatches 189; Indels 138; Gaps
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A40333
collagen alpha 1'(II) chain precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 19-Jul-2004
B;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis em
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 374; Conserv
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trimer;
     skin
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B40333
C.Jolagen alpha 1(II) chain precursor - African clawed frog
C.Species: Xenopus laevis (African clawed frog)
C.Species: Xenopus laevis (African clawed frog)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: B4033
R.Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis (A)
     bovine
C;Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of bovinu 9, 149, 268, and 217 residues.
2, 149, 268, and 217 residues.
2,Comment: The complete chain contains 1052 residues.
C;Superfamily: collagen alpha 1(I) chain, fibrillar collagen carboxyl-terminal hu C;Keywords: coiled coil; extracellular matrix, glycoprotein; pyroglutamic acid, E;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                         148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 GEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGPKGARGSAGPPGATGFPGAAGRVGPP 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPSGNAGPPGPPGPAGKEGSKGPRGETGPAGRPGEVGPPGPPGPAGEKGAPGADGPAGAP 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---K 459
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                                                                                                                                                                                                                                                                                                                                                                                                                        <u>GLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGARGERGFPGERGVBGPPGPAGPRGANGAP</u>
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                                                                                                                                                        Gaps
                                                                                                                    54.4%; Score 1898; DB 1; Length 779;
53.0%; Pred. No. 9.6e-89;
ive 22; Mismatches 210; Indels 108;
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Matches 384; Conservative
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A, Reference number: A40333, MUD: 92011898; PMD: 1918153
A, Accession: B40333
A, Accession: B40333
A, Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: MRNA
A, Residuae: 1-1486 × SUA>
A, Cross-references: UNIPROT: 091718; UNIPROT: 091717; GB: M63595
A, Cross-references: UNIPROT alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; Reywors: coilagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; Reywors: coilagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology vWC>
F;37-96/Domain: Von Willebrand factor type C repeat homology vWC>
F;1258-1486/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                  54.2%; Score 1890.5; DB 1;
.larity 54.6%; Pred. No. 3.6e-88;
Conservative 40; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616
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A;Reference number: A40333, MUID:92011898; PMID:1918153
A;Accession: A40333
A;Accession: A40333
A;Status: nucleic aacid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-142 < SCHA
A;Across-references: UNIPROT:Q91718; UNIPROT:Q91717; GB:M63596
A;Cross-references: UNIPROT:Q91718; UNIPROT:Q91717; GB:M63596
A;Note: this sequence is presented as substitutions relative to another sequence in a files they replace; the appropriate interpretation of the sequence figure was reconstructed Cs.Superfamily: collagen alpha I(T) chain; fibrillar collagen carboxyl-terminal homology; C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix F;37-96/Domain: von Willebrand factor type C repeat homology < VWC>
F;1263-1492/Domain: fibrillar collagen carboxyl-terminal homology < FCC> 13; 331 385 159 51 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGAD-----GVAGPKGPAGERGSPGPAGPK GSPGEAGR PGEAGL PGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVM PGAVGPAGKDGEAGAQGPPGPAGPA GPPGPQGARGFPGTPGLPGVKGHRGYPGLDGGKGEAGAAGAKGESGASGEAGAPGPMGPR Gaps Score 1883; DB 2; Length 1492; Pred. No. 8.6e-88; ; Mismatches 185; Indels 162; GFPGPKGAAGEPGKAGERGVPGP-54.0%; Sccilarity 49.1%; Pre Conservative 46; Similarity Query Match Best Local Simil Matches 379; (332 112 272 52 ò 임 8 d 8

93; 190; Indels DB 2; ; Score 1857.5; DB ; ; Pred. No. 1.6e-86; 39; Mismatches 190 53.3%; Conservative Similarity 369; Query Marc... Best Loca Matches

213 505 273 565 333 625 393 685 411

GARGPEGAOGPRGESGTPGSPGPSGASGNPGTDGIPGAKGSSGASGIAGAPGFPGPRGPP

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GPQGATGPLGPKGETGDPG1AGFKGEHGPKGE1GSAGPQGAPGPAGEEGKRGARGEPGAA GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER GLIGRPGDAGPOGKVGPSGAAGEDGRPGPPGPPGPPGPAGGPGPPGPKGANGEPGKAGEK

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GERGSPGPAGP-

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805

GDÓGVPGEAGAAGLVGPRGERGFPGERGSSGPQGLQGSRGLPGTPGTDGPKGATGPSGPN 745

GLGGAPGLRGLPGKDGETGAQGPNGPAGPRGERGEQGPPGPSGFQGLPGPPGSPGEGGKP

GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP

471 865 513

--- KGSPGEAGRPGEA

573 985

616

GAPGPOGPSGAPGPOGPTGVNGPKGARGAQGPAGATGFPGAAGRVGTPGPNGNPGPPGPP 925

GLPGAKGLTGSPGSPGPDGKTGP-

472 998

g

--PGPAGQDGRPGP---PGPPGAR

GSAGKEGPKGVRGDAGPTGRAGDPGLQGPAGAPGEKGEPGEPGEDGPSGPDGPSGPQGLSGNR

926

셤

574

δ

514

à

GPAGSP-----GFOGLPGPAGPPGEAGKP---GEOGVPGDLGAPGPSGPAG

GQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQ

RESULT 12 S59856 collagen alpha 1(III)

chain precursor

468

GTAGFPGGRGLPGPPGNGNPGPPGPSGAPGKDGPPGPAGNSGSPGNPGIAGPKGDAGQP

GPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP

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A,Molecule type: protein
A,Residues: 87-106;1017-1029;1037-1049 
A,Residues: 87-106;1017-1029;1037-1049 
A,Residues: 87-106;1017-1029;1037-1049 
C,Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are h
C,Comment: The type III collagen molecule is a trimer of identical chains, linked to eac
C,Superfamily: collagen alpha I(I) chain; fibrillar collagen carboxyl-terminal homology;
C,Superfamily: collagen alpha 1(III) chain #status experimental <CAB>
F,1-10449/Product: collagen alpha 1(III) chain #status experimental <CAB>
F,1-10449/Region: amino-terminal nonhelical telopeptide
F,5-87-589/Region: cell attachment (R-G-D) motif
F,587-589/Region: cell attachment (R-G-D) motif
F,878-880/Region: cell attachment (R-G-D) motif
F,878-880/Region: cell attachment (R-G-D) motif
F,9104-1049/Region: cell attachment (R-G-D) motif
F,9104-1049/Region: cell attachment (R-G-D) motif
F,0104-1049/Region: cell a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1041-1049/Region: carboxyl-terminal nonhelical telopeptide
F;95,107,119,938,950/Modified site: 5-hydroxylysine (Lys) #status experimental
F;107,950/Modified site: allysine (Lys) #status predicted
F;107/Binding site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPGGPGLRGIPGSPGGPGSNGKPGPPGSQGETGRPGPPGSPGPRGQPRGQPGVMGFPGPKGND 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GPAGPAGER 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEAGL PGAKGL TGS PG P D GKT G P P G P A G D G P P G P P G P G A G V M G P P G P K G A A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 GAAGPPGPPGSAGTPGLQGMPGERGGPGPGPKGDKGEPGSSGVDGAPGKDGPRGPTGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 GEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGV-----PGDLGAPGPSGPAGEPGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSPGEAGRPGEAGLPGA-----AGLTGSPGSPGPDGKTGPPGP-----AGQDGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912 GPAGPSGAPGPAGSRGPPGPPGPPGPRGPRGETGERGAMGIKGHRGFPGNPGAPGSPGPAGHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          612 GPPGPAGOPGDKGESCAPGVPGIAGPRGGPGBRGEQGPPGPAGFPGAPGONGEPGAKGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.2%; Score 1856; DB 1; Length 1049; 51.2%; Pred. No. 1.5e-86; ive 34; Mismatches '211; Indels 108;

    PGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 51.2
Matches 371; Conservative
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Collagon be primagens taurus (catala catala 
                                                                                                                                                                                                                                                                                                                                            --- PGPAGOD
                                                                                                                                                                         --PGARGQAGVMGFPGPKGAAGE---PGKAGERGVP
                                                                                                                                                                                                                                        989 GERGPPGPQGLPGQPGTAGEPGRDGNPGSDGQPGRDGSPGGKGDRGENGSPGAPGAPGHP
                                                                                                                                                                                                                                                                                                      GPPGAVGPAGXDGE------AGAQGPPGPAGPAGERGEQGPAGSPGFQGLP
                                             ------AGLPGAKGLTGSPGSPGKTGP
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                                                                                                                                                                      GRPGPPGP.
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AjAccession: 8292-423
AjAccession: 8202-423
AjAccession: 8202-423
AjResidues: 302-423
AjResidues: 302-423
AjResidues: 302-423
Aj Accession: 8202-423
Aj Accession: 404-3411, 1978
Ajrile: Covalent structure of collagen: amino acid sequence of five consecutive CNBr p
AjResidues: 399-675, M., 677-727
AjAccession: A90414; MUD:79000343; PMID:687591
AjAccession: A90414; MUD:79000343; PMID:687591
AjAccession: A90414
AjAccession: A90414
AjAccession: A90414; MUD:79000343; PMID:687591
AjAccession: A90414; MUD:79000343; PMID:687591
AjAccession: A90414; MUD:911612; PMID:1672129
AjAccession: 266, 526-5259, 1991
AjTitle: G to T transversion at position +5 of a splice donor site causes skipping of t
AjAccession: 155349
AjAccession: 155349
AjAccession: 155349
AjAccession: 155349
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A;Residues: 965-979, 'A',981-984,'PS',987,'QN',990-1036,'P',1098-1152,'AT',1155,'S',1157
A;Residues: 965-979, 'A',981-984,'PS',987,'QN',990-1036,'P',1098-1152,'AT',1155,'S',1157
B;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; My
Nucleic Acids Res. 12, 9383-9394, 1984
A;Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollag
A;Reference number: A93551; MUID:85087944; PMID:6096827
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A.Residues: 728-895, A'. 197-964 <SEY4>
A.Residues: 728-895, A'. 197-967
B.Experimental source: liver
R.Cole, W.G.; Chiodo A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Cha
A. Blol. Chem. 255, 1070-11071, 1990
A.Title: A base substitution at a splice site in the COL3Al gene causes exon skipping a
A.Reference number: A38303; MUID:91009133; PMID:2145268
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A; Residues: 86-1015 < COL>
A; Residues: 86-1015 < COL>
A; Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PID:
A; Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PID:
A; Mores: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos sy
R; Mankoo, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1988
A; Title: Human pro alpha1(III) collagen: CDNA sequence for the 3' end.
A; Reference number: $02119; MUID:88189827; PMID:3357782
Am. J. Hum. Genet. 53, 62-70, 1993
Ajritle: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual fapring.
Ajritle: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual spring.
Ajritle: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual Ajreference number: IS1868
Ajritle: Parental spread from GB/EMBL/DDBJ
Ajritle: Ajr
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A/Status: translation not shown
A/Status: translation not shown
A/Status: translation
A/Status: Translation
A/Status: Translation
A/Status: 950-1018/Y',1020-1183,'S',1185-1466 < MAN>
A/Status: Translation
B/ACross-raferance: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
R/Seyer, J.M.; Kang, A.H.
Blochemistry 20, 2621-2627, 1981
Blochemistry 20, 2621-2627, 1981
A/Status: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9
A/Status: A90446; MulD:81208139; PMID:7016180
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A, Residues: 1-176 < BEN.>
A, Residues: 1-176 < BEN.>
A, Residues: 1-176 < BEN.>
A, Cross-references: GB.M26939; NID:g180813; PIDN:AAA52040.1; PID:g180814
A, Troman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Nucleic Acids Res. 16, 7201, 1988
A, Title: Acids Res. 16, 7201, 1988
A, Title: Mucleotide sequence of a CDNA coding for the amino-terminal region of human pre A, Reference number: S01726; MUID:88303360; PMID:3405773
A, Accession: S01726
A, Molecule type: MRNA
A, Residues: 1-170 < CDN>
A, Molecule type: MRNA
A, Residues: 1-170 < CDN>
A, Molecule type: MRNA
A, Residues: 1-170 < CDN>
A, Molecule type: MRNA
A, Residue 154 as His
R, Manirez, F.
Nucleic Acids Res. 17, 6742, 1989
A, Mittle: Nuclectide and amino acid sequences of the entire human alpha-1 (III) collagen.
A, Accession: S04887; MUID:89386015; PMID:2780304
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*NOTE: He authors' translation of residues 905-932 is inconsistent with the nucleotide spectral translation of residues 905-932 is inconsistent with the nucleotide sochemistry 16, 1188-1164, 1977

*Note: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide specific translation: A90399; MUID:77134724; PMID:557335
                                                                                                                                                                                                                                                                                                                                                                                                                                              October alpha 1(III) chain precursor - human NyAlternate names: procollagen alpha 1(III) chain (Species to Ames: procollagen alpha 1(III) chain (Species to Ames: procollagen alpha 1(III) chain (Species to Ames: procollagen alpha 1(III) chain (Species to Southern the man sapiens (man) (Species to Southern the Ames to Southern the American (Southern to American to The Embl. Data Library, February 1989 (Species to The Embl. Data Library, February 1989 (Species to The Embl. Southern the American to Southern the American to Southern the American the 
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A,Note: sequence corrected by A94562; attachment of 2-0-alpha-D-glucosyl-O-beta-D-galact
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submitted to the Atlas, December 1977
AjReference number: A94562
AjMolecule type: protein
AjRecession: A94562
AjRecession: A94562
AjResidues: 'V'.169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
AjExperimental source: liver
AjResidues: 'W'.169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
AjExperimental source: liver
AjNote: author submitted corrections to A90399
RjMilewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
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A; Residues: 1-1196 <-ALA>
A; Residues: 1-1196 <-ALA>
A; Cross-references: EMBi; X14420; NID:g330557; PIDN:CAA32583.1; PID:g33058
A; Cross-references: EMBi; X14420; NID:g330557; PIDN:CAA32583.1; PID:g33058
A; Cross-reference complete sequence is not shown
R; Renson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
Gene 78, 255-265, 1989
A; Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene
A; Reference number: PE0011; MUID:89378752; PMID:2777083
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A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEY1>
A;Experimental source: liver
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GPPG 1035
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from

587

210

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312

827

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A,Residues: 1-886 <NAH>
A,Cross-references: UNIPROT:P12105, EMBL:U07973; NID:g520454; PIDN:AAA83407.1; PID:g5374
C,Genetics:
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R;Nah, H.D.; Niu, Z.; Adams, S.L.
J. Biol. Chem. 269, 16443-16448, 1994
A;Title: An alternative transcript of the chick type III collagen gene that does not A;Reference number: A54041; MUID:94266842; PMID:8206952
A;Accession: IS6694
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           948 GIAGITGARGLAGPPGMPGPRGSPGPQGVKGESGKPGANGLSGERGPPGPQGLPGLAGTA 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .008 GEPGRDGNPGSDGLPGRDGSPGGKGDRGENGSPGAPGAPGAPGPPGPVGPAGKSGDRGES 1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           648 GPPGENGKPGEPGPKGDAGAPGAPGKGDAGAPGERGPPGLAGAPGLRGGAGPPGPEGGK 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GV---MGFPGPKGAAGEPGKAGERGVPGP-------PGAVGPAGKDGEA 351
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                                                                                                                 528 GVPGGPGWRGMPGSPGGPGSDGKPGPPGSQGESGRPGPPGPSGPRGQPGVMGFPGPVGND
                                                                       GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA
                                                                                                                                                                                                                               121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                               588 GAPGKNGERGGPGGPPGKNGETGPQGPPGPTGPGGDKGDTGPPGPQGLQGLPGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           768 GPPGPAGQPGDKGEGGAPGLPGIAGPRGSPGERGETGPPGPAGFPGAPGONGEPGGKGER
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A; Molecule type: mRNA
A; Residues: 165-1155, P., 1157-1466 cLOI>
A; Cross-references: EMBL.X01655; EMBL.X0142; NID:929584; PIDN:CAA25821.1
R; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant
Biochemistry 25, 1403-1413, 1986
A; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant
Biochemistry 25, 1403-1413, 1986
A; Accession: 15293; MUID:86187804; PMID:3754462
A; Accession: 15293
A; Readus: translated from GB/EMBL/DDBJ
A; Readus: translated from GB/EMBL/DDBJ
A; Reference number: 159025; MUID:85216505; PMID:3858826
A; A; Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
A; Reference number: 159025; MUID:85216505; PMID:3858826
A; A; Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
A; Residues: 1165-1196 ARMA

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3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently C (Genetics)
A,Genetics.
A,Genetics.
C,Genetics.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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2; Mismatches 209;
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11; Gaps / Match 52.8%; Score 1840; DB 2; Length 886; Local Similarity 49.8%; Pred. No. 8.4e-86; nes 362; Conservative 44; Mismatches 195; Indels 126; Query Match Best Local Simil Matches 362; C

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries UniProt_02:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

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ALIGNMENTS

RESULT 1

1825181

Total number of hits satisfying chosen parameters:

1825181 segs, 575374646 residues

Searched:

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PubMed=3857621;
Barsh G.S., Roush C.L., Bonadio J., Byers P.H., Gelinas R.E.;
Barsh G.S., Roush C.L., Bonadio J., Byers P.H., Gelinas R.E.;
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Proc. Natl. Acad. Sci. U.S.A. 82:2870-2874 [1985].
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MEDLINE-93352646; PubMed=8434697;
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"Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of type I collagen result in defective chain association and produce lethal osteogenesis imperfecta.";
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Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.;
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Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).
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Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
"A comparative study of glycopeptides derived from selected vertebrate
Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F., Prockop D.J., "Nucleotide sequences of complementary deoxyribonucleic acids for the pro alpha 1 chain of human type I procollagen. Statistical evaluation of structures that are conserved during evolution."; Biochemistry 22:5213-5223(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85130970; PubMed=2857713;
Chu M.-L., de Wet W., Bernard M.P., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
"Promoter structure, AluI repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
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Hunan pro alpha 1(1) collagen: cDNA sequence for the C-propeptide
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Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez
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increased type III collagen mRNA.";
J. Biol. Chem. 260:691-694(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Specific cleavage site at residue Leu95.";
Eur. J. Biochem. 192:153-159(1990).
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J. Biol. Chem. 262:15151-15157(1987).
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J. Biol. Chem. 268:18218-18225(1993).
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Wallis G.A., Starman B.J., Zinn A.B., Byers P.H.,
"Variable expression of osteogenesis imperfecta in a nuclear family is
explained by somatic mesaicism for a lethal point mutation in the
alpha 1(1) gene (COLIAN) of type I collagen in a parent.";
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MEDLINE=91184577; PubMed=2010058;
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"Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 425-490; 965-1024; 999-1039 AND 1453-1464 FROM N.A. MEDLINE=83064528; PubMed=6183642; Chu M.-L., Myers J.C., Bernard M.P., Ding J.-F., Ramirez F.; "Cloning and characterization of five overlapping cDNAs specific for the human pro alpha 1(1) collagen chain."; Nucleic Acids Res. 10:5925-5934(1982).
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1143-1162 FROM N.A.
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PubMed=3170557;
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FASEB J. 5:2052-2060(1991).
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"Fine structural analysis of the human pro-alpha 1 (1) collagen gene.
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J. Biol. Chem. 260:2315-2320(1985).
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Ala-Kokko J.M., Earley J.J., Nuytinck L., DePaepe A., Prockop D.J.,
Ala-Kokko L.;
Submitted (Mrx-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, ARC11/T8; AAB94054.2; -
GO; GO:0005581; C:collagen; IEA.
GO; GO:0005573; C:cytoplasm; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008161; Clg helix.
InterPro; IPR008165; Collagen.
InterPro; IPR001077; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98107942; PubMed=9443882; MEDLINE=98107942; PubMed=9443882; MEDLINE=98107942; PubMed=9443882; Meditor I., Barley J., Prockop D.J.; Ala-Kokko L., De Paepe A., Nuytinck L., Earley J., Prockop D.J.; Ala-Koklal and COLIA2 genes by PCR amplification and scanning by conformation-sensitive gel electrophoresis identifies COLIA1 mutations in 15 patients with osteogenesis imperfecta type identification of comon sequences of null-allele mutations."; Am. J. Hum. Genet. 62:98-110(1998).
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJUNE=89025644; PubMed=3178743; Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T., Jaenisch R., Prockop D.J.; Structure of a full-length cDNA clone for the prepro alpha 1(1) of human type I procollagen."; Biochem. J. 253:919-922(1988).
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=88329734; PubMed=2843432;
D'Alessio M., Bernard M., Pretorius P.J., de Wet W., Ramirez F.
"Complete nucleotide sequence of the region encompassing the fit
twenty-five exons of the human pro alpha 1(1) collagen gene.",
Gene 67:105-115(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. PubMed=1787829; MansDLINE=29157916; PubMed=1787829; Mesterhausen A., Constantinou C.D., Pack M., Peng M.Z., Ham Olsen A.S., Prockop D.J.; "Completion of the last half of the structure of the human the Pro alpha I (I) chain of type I procollagen (COLIAI)."; Matrix II:375-379(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91138770; PubMed=1995349;
Matta A., Bornstein P., Pentinen R.P.;
"Highly conserved sequences in the 3'-untranslated COLIA1 gene bind cell-specific nuclear proteins.";
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PÉan; PFO1391; COLFI; 1.
PEODOM; PD000007; C1g_helix; 3.
PEODOM; PD002078; Fib_collagen_C; SMART; SM00218; VWC; 1.
PROSITE; PS01268; VWC; 1; 1.
PROSITE; PS01268; VWFC 1; 1.
                              SEQUENCE FROM N.A.
MEDLINE=85130970; PubMed=2857713;
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Catarrhini; Hominidae; Homo.
                                                                                   Length 1464;
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Last annotation update)
                                                                                   DB 1;
                                                                          64.1%; Score 2237.5; DB 1; 60.2%; Pred. No. 9.5e-83; ive 23; Mismatches 152;
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REVIEW ON OI VARIANTS.
MEDLINE=91374476; PubMed=1895312;
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Mammalia, Eutheria, Primates,
NCBI_TaxID=9606;
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076045 01-NOV-1998 (TrEMBLEEL 12, L
01-NOV-1999 (TrEMBLEEL 12, L
01-NOV-1999 (TrEMBLEEL 26, L
Pro alpha 1(1) collagen.
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Best Local Similarity 60.2<sup>§</sup>
Matches 441, Conservative
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SMART; SM00214; VWC; 1.
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                                                                                      -----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Pred. No. 1.4e-82;
3; Mismatches 153; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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MEDLINE=22388257; PubMed=12477932;
llarity 60.0%; Pr
Conservative 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1175 GPPGPPGPPGPPG 1187
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Best Local Similarity
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12; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Schaenen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Dalchenhok L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loqquellano N.A., Peters G.J., Abzamson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Mnizhy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., 458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 517 108 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 577 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 637 697 48 Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human EMBL; BC036531; AAH36531.1; ...

EMBL; BC036531; AAH36531.1; ...

GO; GO:0005231; C:collagen; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

GO; GO:0006217; P:phosphate transport; IEA.

R GO; GO:0006817; P:phosphate transport; IEA.

InterPro; IPR003161; Clg_helix.

R InterPro; IPR00385; Fib collagen.

R InterPro; IPR003961; VWFC.

R InterPro; IPR003041; VWFC.

R Pfam; PF01410; CoLFT; 1.

R Pfam; PF01410; CoLFT; 1.

R Pfam; PF01410; CoLFT; 1.

R Probom; PD00007; Clg_helix; 3. GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDCEAGAQGPPGPAGEAGERGEQGPA GSPGFQGLPGPAGPPGBAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA ----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP 698 GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP Gaps 117; Length 1464; 'Match 64.0%; Score 2233.5; DB 2; Length Local Similarity 60.0%; Pred. No. 1.4e-82; les 440; Conservative 23; Mismatches 153; Indels Strausberg R.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). B0581F8D1C89DDE8

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GVMGFPGPXGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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Nonhelical region (N-terminal).

Triple-belical region (N-terminal).

Triple-belical region (C-terminal).

Nonhelical region (C-terminal).

Cell attachment site (Potential).

Cell attachment site (Potential).

Pyrrolidone carboxylic acid (By similarity).

Allysine (By similarity).

5-hydroxylysine (By similarity).

7-hydroxylysine (By similarity).

6-linked (Gal. .) (By similarity).

C-linked (Gal. .) (By similarity).

G-> A (in OI; severe).

G-> A (in OI; severe).
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                                                                                                                                                           Disease mutation; Extracellular matrix;
                                                                                                                                                                          Pyrrolidone carboxylic acid; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.0%; Score 2231.5; DB 1; Length 1460; 60.2%; Pred. No. 1.7e-82; ive 20; Mismatches 155; Indels 117;
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N-terminal propeptide.
Collagen alpha 1(1) chain.
C-terminal propeptide.
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InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR01007; VWF_C.
Pfam; PF01410; CoLF1; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Clg_helix; 2.
ProDom; PD00007; Clg_helix; 2.
ProDom; PD000078; Fib_collagen_C; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
Collagen; Connective Lissue; Disease m
                                                                                                                                               M Glycoprotein; Hydroxylation; Pyl Signal.
T Signal.
T PROPED 23 157 N-t.
PROPED 128 1214 Coll.
PROPED 1218 1214 Coll.
PROPED 131 92 VWPC
DOMAIN 158 174 Nonh.
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1460 AA; 138762
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                                                                                                                                                                                                                                                                                                                                                                               GPAGKSGDRGETGPAGPAGPVGPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1117
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GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRIGDAGPV 1177
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                             GPPGPPGARGQ------AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
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-1- SIMILARITY: Contains 1 VWFC domain.
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(I) chain precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659 GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP 718
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NAt. Genet. 15:99-98(1997).

NAT. EMBL, X98705; CAA6726.1; -
                                                                                                                                                                                    419 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGFKGSPGEAGRPGEAGLPGAK
                                                                                                                                                             214 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                                                                                                                                                         539 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEFGKAGER
                                                                GPPGEAGKPGEQGVPGDLGAP-------GEPGPA-----GEPGPT
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57.6%; Pred. No. 3.3e-82;
ive 17; Mismatches 151; Indels 162; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Collagen type I alpha I (Fragment).
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994 GPMGPPGLAGPPGESGREGSPGAEGSPGRDGSPGPKGDRGETGPAGPPGAPGAPGAV 1053
                                                                                                                                       ---AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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MEDIJNE=97141927; PubMed=8988177;
Simon M., Pedeutour F., O'Srien K., Sirvent N., Kedra D., Guilbaud C
Simon M., Pedeutour F., O'Brien K., Sirvent M., Kedra D., Guilbaud C
Turc-Carel C., Dumanski J.P.;
"Regulation of the platelet-derived growth factor B-chain gene via
fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans
and giant-cell fibroblastoma.";
Nat. Genet. 15:95-98(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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llarity 57.6%; Pred. No. 3.3e-82;
Conservative 17; Mismatches 151; Indels 162;
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Lubmitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

R InterPro; IPRO08161; Clg helix.

InterPro; IPRO08161; Clg helix.

InterPro; IPRO08161; Clg helix.

InterPro; IPRO09161; PMP SGCI.

R InterPro; IPRO01007; VWF_C.

Pfam; PF01391; Collagen; 15.

R ProDom; PD000007; Clg helix; 3.

R ProDom; PD000007; Clg helix; 3.

R PROSITE; PSS0184; VWFC_1; 1.

PROSITE; PSS0184; VWFC_2; 1.
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                                            GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE--
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Collagen type I alpha 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1069 AA
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Matches 448; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.5%; Score 2215.5; DB 2;
Best Local Similarity 53.8%; Pred. No. 7.2e-82;
Matches 446; Conservative 21; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GPPGE---PGPTGLPGPPGERGGPGSRGFPG-----
GO; GO:0006817; P:phosphate transport; IEA
              InterPro; IPR00816; Collagen.
InterPro; IPR00816; Collagen.
InterPro; IPR00816; Collagen.
InterPro; IPR00816; Fib collagen.
InterPro; IPR009041; PWP_CGI.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; Collagen; 18.
ProDom; PD000070; Clg_helix; 3.
ProDom; PD002078; Fib collagen_C; I.
SWART; SM00214; VWF_C; I.
PROSITE; PS50126; VWF_C; I.
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MEDLINE=99163824; PubMed=10065941;
MEDLINE=99163824; PubMed=10065941;
Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
Expression of collagen alphal(I) mRNA variants during tooth and bone formation in the rat.";

formation in the rat.";

ENBL, 278279; CAB016331; -1600, CO.0005581; Co.01agen; IRA.

GO, GO:0005781; C:collagen; IRA.

GO, GO:0005737; C:cytoplasm; IRA.

GO; GO:0005737; C:cytoplasm; IRA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
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                               GRPGERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAP
                                                                                                                                                   GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPPGPPGPPGAVGAXGEAGPQ
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-JUN-1998 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Collagen alphal (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muxinae; Rattus.
                                                                                                           GOAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------
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213 -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPKGSP
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CAA29927.1,
AAA37332.1;
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AAA37332.1;
AAA37332.1;
AAA37332.1;
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K03034; AAA37332.1;
K03035; AAA37332.1;
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K03036;
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K03032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88124276; PubMed=3340560;
MEDLINE=88124276; PubMed=3340560;
Mooslehner K., Harbers K.,
"Two mRNAs of mouse pro alpha 1(1) collagen gene differ in the size of the 3'-untranslated region.";
Nucleic Acids Res. 16:773-773(1988).
-!- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
-!- SUBUNIT: Trimers of one alpha 2(1) and two alpha 1(1) chains.
-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 518-1128 FROM N.A. MEDLINES.66.31403; WHOLLINES.66.13403; W.D.Mode3.8415.23; French B.T., Lee W.-H., Maul G.G.; "Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I) collagen
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96033240; PubMed=8535610;
Li S. W., Khillan J., Prockop D.J.;
"The complete CDM coding sequence for the mouse pro alpha 1(I) chain
of type I procollagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 735-1130 FROM N.A.
MEDLINE-83141374; PubMed-6298597;
MROSON J.M., Friedman J., McCarthy B.J.;
"DNA sequence analysis of a mouse pro alpha 1 (I) procollagen gene: evidence for a mouse B. I element within the gene.";
Mol. Cell. Biol. 2:1362-1371(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 WWFC domain.
                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
MEDLINE-83157109; PubMed-6219867;
Monson J.M., McCarthy B.J.;
"Identification of a Balb/c mouse pro alpha 1(I) procollagen gene:
evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
             568 GERGEQGPAGSPGFPGEPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 616
                                              897 GPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGSPGTPGPQGIAG 945
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                                                                                                                                            PRT; 1453 AA
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                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 39:311-312(1985)
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=FVB/N
                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.";
                                                                                                                         MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).

Allyaine (By similarity).

5-hydroxylysine (By similarity).

3-hydroxyproline (By similarity).

N-linked (GlonAc. ) (Potential).

N-linked (GlonAc. ) (By similarity).

N-linked (GlonAc. ) (By similarity).

Cell attachment site (Potential).

A -> v (in Ref. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPP------GEPGPTGLPGPPGBRGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           567 GVMGFPGPKGTAGEPGKAGERGLPGPPGAVGPAGKDGEAGAQGAPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPAGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
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PIR; S5743; S1626.

R MGD; MGI:88467; Colla1.

R InterPro; IPR008160; Collagen.

R InterPro; IPR008160; Collagen.

R InterPro; IPR00911; PMP_SGGI.

R InterPro; IPR0091007; VWF_C.

R Ffam; PF01410; COLFI; 1.

R Probom; PD002078; Fib_collagen, IS.

R Probom; PD002078; Fib_collagen, IS.

R SWART; SM00214; VWC; 1.

R SWART; SM00214; VWC; 1.

R RP03ITE; PS01284; VWC; 1.

R COllagen; Connective tissue; Extracellular matrix; Glycoprotein; W Hydroxylation; Pyrrolidone carboxylic acid; Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 2205.5; DB 1; Length 1453;
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Nonhelical region (C-terminal).
Pyrrolidone carboxylic acid (By
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ive 22; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137944 MW; 3B802E535DF81808 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-terminal propeptide.
Collagen alpha 1(I) chain.
C-terminal propeptide.
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454 GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                Strainghouse Strai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPAGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 687 GNNGAPGNDGAKGDTGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDRGPKGADGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              867 GAAGRVGPPGPSGNAGPPGPPGPVGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.2%; Score 2205.5; DB 2; Length 1453; Best Local Similarity 58.9%; Pred. No. 1.8e-81; Matches 432; Conservative 22; Mismatches 162; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1453 AA; 138032 MW; 0B7F06BBB9A1D5EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO1208; VWFC_1; 1.
PROSITE; PSS0184; VWFC_2; 1.
Collagen.
SEQUENCE 1453 AA; 138032 |
  [2]
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPGPPGARGQ-----
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SECURENCE FROW N.N.

STATANS-E7388257; PubMed=12477912;

NEDLINE=22388257; PubMed=12477912;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A lusoner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A lustchento S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A lustchento L., Marusina K.N., Farmer A.A., Rubin G.M., Hong L.,

A batchento L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R. And S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gubbs R.A.,

R. Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gubbs R.A.,

R. Hallalon D.K., Muzny D.M., Sodergran B.J., Lu X., Gibbs R.A.,

R. Pahey J., Helton B., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Razywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1047 GPAGKNGDRGETGPAGPAGPIGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1106
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                                                                                                                                                                                                                                                                        ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                                                                                                                                                                     GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
GNNGAPGNDGAKGDTGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDKGDAGPKGADGSP
                                                                                                                                                                                                                                                                                                                                                                                                                       GADGPAGSPGTPGPQGTAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGSSGERGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP
                                                                             ----AGRPGEAGLPGAKGLTGSPGSPGPD-----GKTGPPGPAGQDGRP
                                                                                                                         GKDGARGLTGPIGPPGPAGAPGDKGEAGPSGPPGPTGARGAPGDRGEAGPPGPAGPP
                                                                                                                                                                                ---AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0810J9;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUNR-2004 (TrEMBLrel. 26, Last annotation update)
Procollagen, type I, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GARGQAGVMGFPGPKGAAGEPGKAGERGVPGP------
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1167 GPPGPPGPPGPPG 1179
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                                                                                                                                                                                GPPGPPGARGO-
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117860 MW; B6B86CBB4457F4D9 CRC64;
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02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
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     1225 AA;
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     SEQUENCE
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TISSUE-Mammary tunnor. WAP-TGF alpha model. 7 months old;

X TISSUE-Mammary tunnor. WAP-TGF alpha model. 7 months old;

X MEDINE-22388257; PubMed=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,

A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Datchenko L., Modin T.B., Toshiyuki S., Carninoi P., Prange C.,

A Brownstein M.J., Uodin T.B., Toshiyuki S., Carninoi P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Robards S. Worler W.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Milandon D.K., Muzny D.M., Sodarcia A.M., Gay L.J., Hulyk S.W.,

A Milandon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A.,

A Nillandon A., Young A.C., Shevchenko Y., Boutfard G.G.,

A Nilland A., Youchman J.W., Green B.D., Dickson M.C.,

A Richaels R.W., Touchman J.W., Green B.D., Dickson M.C.,

A Richaels M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                            547 GPACKDGBAGAQGPPGPAGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC059281; AAH59281.1; ...

InterPro; IPR008160; Cilagen.

InterPro; IPR008181; Fibrinogen_C.

InterPro; IPR008081; Pibrinogen_C.

InterPro; IPR008081; Pibrinogen_C.

InterPro; IPR008081; Pibrinogen_C.

InterPro; IPR001007; VWF_C.

Pfam; PF01991; Collagen; 14.

Pfam; PF01991; Collagen; 14.

Probom; PD00007; Cig helix; 2.

Probom; PD00007; Cig helix; 2.

SWART; SM00038; COLFI; 1.
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STRAIN=Mix FVB/N,
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                  604 GDLGAPGPSGPAG 616
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
Collal protein.
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Mus musculus (Mouse).
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SEQUENCE FROM N.A.
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Query Match 62.4%; Score 2176.5; DB 2; Length 1225; Best Local Similarity 56.7%; Pred. No. 2.4e-80; Matches 431; Conservative 28; Mismatches 157; Indels 144; Gaps
                                                                                                                                                  1 GPPGEPGPTGLPGPPGE-------RGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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Mammalia, Eutherla, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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             MEDIAINE-25386257; PubMed=1247732;

A Klausher R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Klausher R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

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A Altschul S.F., Jozdan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Rabey J., Helton E., Ketteman M., Madan A.M., Rodrigues S., Sanchez A.,

Bhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ry Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Ry Monte S.J., Marra M.A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stransberg R.; Stransberg R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC059281; AAH59281.1; -. SEOUENCE 1225 AA; 117860 NW; BCB86CBB4457F4D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2] SEQUENCE FROM N.A. STRAIN=CS7BL/6J; TISSUE=Mammary tumor;
STRAIN=C57BL/6J; TISSUE=Mammary tumor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
Proc. Natl. Acad. Sci. U.
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Best Local Similarity
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MEDLINE-82231995; PubMed=7093229;
Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H.,
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MEDLINE=72243016; PubMed=5047697;

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GPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAV
                                                                         GPAGKDGEAGAQGPPGPAGPAGERGE------QGPAGSPGFQGLPGPA----
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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MEDLINE=80134546; PubMed=6987088;
Showalter A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T.,
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MEDLINE=88056316; PubMed=3678834;
Finer M.H., Boedtker H., Doty P.;
"Construction and characterization of cDNA clones encoding the 'Gonstruction and characterization of cDNA clones Gene Cof the chicken pro alpha 1(I) collagen mRNA.";
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MEDLINE=88007542; PubMed=2820966;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., and S. Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., and S. Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M. Sequences located within the promoter region and first intron of the chicken pro-alpha 1(I) collagen gene.";
J. Biol. Chem. 262:13323-13332(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 GPRGPPGSAGSPGKDGLNGLPGPIGPPGPRGRTGDSGPAG 939
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01-OCT-1989 (Rel. 12, Last sequence update)
COLT-2004 (Rel. 45, Last annotation update)
COLlagen alpha 1(I) chain precursor.
Name=COLIA1;
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MEDLINE=81160715; PubMed=6927845;
Fuller F., Boedtker H.;
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212

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806

998 393 926 453

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987 GPMGPPGLAGPPGEAGREGAPGAEGAPGRDGAAGPKGDRGETGPAGPPGAPGAPGAPGPV 1046
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                                                                                                                                                                                                          GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                  567 GVMGFFGPKGAAGBPGKPGEKGAPGPPGAVGAAGKDGBAGAQGPPGPTGPAGEKGEQGPA
                                                                                                             GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----
                                                                                                                                              627 GAPGFOGLPGPAGPPGEAGKPGEQGVPGNAGAPGPAGARGERGFPGERGVQGPPGPR
                                                                                                                                                                                                                                                                                                                                                                                                  337 GPPGAVGPAGKDGBAGAQGPPGPAGPAGPAGE---RGEQGPAGSPGFQGLPGPAGPPGEAGKP
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                                                                                                                                                                                                                                                        -----AGPKGSPGEAGRP---GEAGLPGAKGLTGSPGSPGPDGKTGPPGPA----
                                                                                                                                                                                                                                                                                          747 GKDGLRGLTGPIGPPGPAGAPGDKGEAGPPGPAGPTGARGAPGDRGEPGPPGPAGFAGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                    -------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGP
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01-MAY-1999
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                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the between the Swiss Institute of Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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               -1- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
-1- SUBUNIT: Trainers of one alpha 2(I) and two alpha 1(I) chains.
-1- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 Allyaine (By Similarity).
254 5-hydroxylysine (By similarity).
255 5-hydroxylysine (By similarity).
1081 Fydroxylysine (Potential).
1153 3-hydroxylysine (Potential).
254 0-linked (Gal.,) (By similarity).
1187 P.-L (In Ref. 5).
1187 P.-L (In Ref. 5).
1187 P.-L (In Ref. 5).
1187 P.-L (In Ref. 6).
1187 P.-H (In Ref. 6).
1187 P.-H (In Ref. 6).
                                                                                                                       PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X. Brintaratry: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.7%; Score 2151.5; DB 1; Length 1453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collagen; Connective tīssue; Direct protein sequencing;
Extracellular matrix; Glycoprotein; Hydroxylation;
Pyrrolidone carboxylic acid; Repeat; Signal.
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Collagen alpha 1(I) cha
C-terminal propeptide.
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InterPro; IPR008160; Collagen.
InterPro; IPR000885; Fib collagen_C.
InterPro; IPR001007; VWF_C.
Fam; PF01410; CoLF1; 1.
Pfam; PF01391; Collagen; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000007; Clg_helix; 2.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; CCLFI; 1.
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EMBL, M17838; AAA48704.1; JOINED.
EMBL, VOOA01; CAA23895.1; --
EMBL, M10571; AAA48671.1; ALT_SEQ.
EMBL, M17670; AAA48672.1; --
PIR, A27179; A27179
PIR, 150629; ISO629.
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PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%;
Lett. 111:61-65(1980)
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                                                                                                          hydroxyapatite.
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CARBOHYD
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MOD RES
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------558

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Cynops pyrrhogaster (Japanese common newt).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae, Cynops.
NCBI_TaxID=8330;
            PRT; 1450 AA.
                                                                                                                                    GO; GO: 0005737; C:cytoplasm; IEP
GO; GO: 0005201; F:extracellular
GO; GO: 0006817; P:phosphate trai
InterPro; IPR008161; Clg_helix.
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GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQDGRPGPPGPRGARGQA 108

49

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|||| |447 GPPGPAGEEGKRGÅRGEPGPAGLPGPAGERGAPGSRGFPGADGIAGPKGPPGERGSPGAV 506 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA

PRT; 1445 AA

PRELIMINARY;

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151
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                                                                                                                                                                                                                                                                                                                                                                                        503
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                                                                                                                                                                                                                                                                                                                                                   48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 GVMGFPGPKGAAGEPGKSGERGVAGPPGATGAPGKDGEAGAQGPPGFSGPSGEKGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGPTGLPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 GSPGFQGLPGSPGPAGEAGKPGEQGAPGDAGGPGPSGPRGFRGFPGERGGPGPPGAQGPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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                                                                                                                                                                                                                                    1450 AA; 137563 MW; ABF8A74841B87B7C CRC64;
InterPro; IPR008160; Collagen.
InterPro; IPR001805; Fib_collagen_C.
InterPro; IPR01007; VWF_C.
Pfam; PF01391; CoLF1; 1.
ProDom; PD00007; Clagen: 18.
ProDom; P0002078; Fib_collagen_C; 1.
SWART; SW0018; Fib_collagen_C; 1.
PROSITE; P801208; VWFC 1; 1.
PROSITE; P851208; VWFC 1; UNKNOWN_1.
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                                                                                                                                                                                                                      Collagen.
SEQUENCE
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RESULT 14 093251

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                                                                                                                                                                                                                                                                                    PSEQUENCE FROW N.A.

MEDLINE=99294154; PubMed=10367734;

Asahina K., Utoh R., Obara M., Yoshizato K.;

Tr. of al(I) and a2(I) collagen in intestine duting

amphibianmetamorphosis.";

In Matrix Biol. 18:99-103(1999).

EMBL; ABOIL440; BB-103(1999).

RO; GO:0005591; C:cytoplasen; IEA.

GO; GO:0005591; C:cytoplasen; IEA.

GO; GO:0005591; C:cytoplasen; IEA.

GO; GO:000581; P:extracellular matrix structural constituent; IEA.

GO; GO:000581; P:extracellular matrix

GO; GO:000581; P:extracellular.

InterPro; IPR008161; Golfagen.

RINTERPO; IPR008161; Golfagen.

RINTERPO; IPR001007; WF_C.

REPOM; PD000007; C1g helix: 4.

REMRT; SM00038; Fib_collagen_C; 1.

SMART; SM00038; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 GAPGPQGPGGSPGPKGNNGEPGAQGNKGEPGAKGESGPAGSQGPPGPPGEEGKRGSRGEP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLP 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NON-1998 (TrEMBLrel. 26, Last annotation update)
Alpha 1 type I collagen.
Name=alpha 1 type I collagen;
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

58.6%; Score 2042.5; DB 2; Length

Best Local Similarity 49.7%; Pred. No. 6.2e-75;

Matches 421; Conservative 34; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPPGEPGPTGLPGPPGERGGPGS------RGFPGADGVAGPKGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1445 AA; 137251 MW; F59BB550C9873F04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LGAPGPSGP
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PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKPGEQGVPGD---
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collagen.
SEQUENCE
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ProDom, PD002078; Fib_collagen_C; 1.
SMART; SM0038; COLFI; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
Collagen.
                                                                                                                                                                                                                      1449 AA; 137464 MW;
                        Dev. Dyn. 225:384-391(2002)
                                       FROM N.A.
  Richardson P.;
                                               FISSUE=Embryo;
                                [3]
SEQUENCE
                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            226
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                                                        GKPGEQGAPGDVGPSGPAGSRGERGPPGERGAIGPPGPQGPRGANGAPGNDGAKGEAGAP
                                               -- KGS PGEAGRP
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                                                                                                           -GPAGQDGRP---GPPGP-----PGARGQAGVMGFPGPKGAA
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MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                -GP-GSRGFPGADGV
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                             GEAGLPGAKGLTGSP------
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Xenopus laevis (African clawed frog)
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Klein S., Strausberg R.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

R GO198019 AAH498291;

R GO1 GO1005513; C:cytoplasm; IEA.

R GO1 GO1005513; C:cytoplasm; IEA.

R GO1 GO1005513; C:cytoplasm; IEA.

R GO1 GO1005513; P:phosphate transport; IEA.

R GO1 GO1006517; P:phosphate transport; IEA.

R HEEPRO; IPR001007; VWF.C.

R Fam; PF01191; COLFI: 1.

R Fam; PF001391; Collagen; IB.

DR ProDom; PD000007; CIQ-helix; 4.

P ProDom; PD000007; CIQ-helix; 4.
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"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.", % \left( \frac{1}{2}\right) =\left( \frac{1}{2}\right) +\left( 
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Search completed: October 18, 2004, 13:41:50 Job time: 117.271 secs

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GenCore version 5.16

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OM protein - protein search, using sw model

Run on:
October 18, 2004, 13:22:25; Search time 129:602 Seconds
(without alignments)
2272.479 Million cell updates/sec
Perfect score: 4640
Sequence:
1 GPPGEPQFTGLPGPPGERGG.......GEQGVPGDLGAPGPSGPAGG 821
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273
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Database: A Geneseq_23Sep04:*

1: __geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
7: geneseqp2003as:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
8: geneseqp2003bs:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adm48392 Human r	1 Human	17	535 Porcine	544 A huma	103 Amino	540	38	5 Human	5059 Human	5055 Human	21	47 Human	136	-	Aay84539 Amino aci	4 Human	4	App68610 Human pan	Abu54471 Human tum	7 Breast	64 Human	Add14142 Human src	246 Human	9470 Human
SUMMARIES		ADM48392	6	ADQ26217	AAE02535	AAY84544	AAY84403	AAY84540	AAY84538	AAW68485	ADD45059	ADD45055	ADD45051	ABG93947	AAU14136	AAY84541	AAY84539	AAB82454	ABB90764	ABP68610	ABU54471	ABR47417	ABR92064	ADD14142	ADP65246	ADQ19470
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Aae02532 Bovine al	Ade87048 Human pan	Aar89472 Collagen/	Aar89469 Collagen/	Aay84537 Amino aci	Aar89470 Collagen/	0011		Add45057 Rat Prote	Add48341 Rat Prote	Rat	Rat	Add48345 Rat Prote	Abg93948 Mouse pol	Human	Aay56800 Human pre	Ade87062 Human pan		Aay96122 Collagen	Aae16475 Human col	
AAE02532	ADE87048	AAR89472	AAR89469	AAY84537	AAR89470	AAR89471	ADD45053	ADD45057	ADD48341	ADD45049	ADD48337	ADD48345	ABG93948	ADE87051	AAY56800	ADE87062	ABG22679	AAY96122	AAE16475	
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ALIGNMENTS

RESULT ADM483 ID A	ADM48392 ID ADM48392 standard; protein; 821 AA. XX	
{	ADM48392;	
1	03-JUN-2004 (first entry)	
18	Human recombinant gelatin-like polypeptide Hu-4.	
≨ ≩}	Plasma substitute; Gelatin-like protein; plasma expander; human.	
88	Homo sapiens.	
A E	EP1398324-A1.	
X E	17-MAR-2004.	
X E	11-SEP-2002; 2002EP-00078745.	
X K	11-SEP-2002; 2002EP-00078745.	
Y &	(FUJF) FUJI PHOTO FILM BV.	
X II I	Bouwstra JB, Toda Y;	
ž K	WPI; 2004-229415/22.	
PT	Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function.	
8 K	Example 1; SEQ ID NO 3; 31pp; English.	
388	in sequence of recombinant gelatin-li of human recombinant gelatin-like	
ខ្លួ	protein Hu-1 ADW48390. A claimed composition suitable as a substitute for	
38	The protein i	
ប្តប្	a molecular Weight of at least 10 Aba and at most 30 Aba and at isoelectric point of less than 8. It is especially Hu-1 or Hu-deam	
888	gelatin-like s useful as	
388	clearance rate from blood circulation, provides better and predictable	
ខ្លួ	regulation of clearance rate and which is recomplications describing defaulth-degradation than presently used gelatin-	
ខ្លួ	ls that are in essence free or mylloxyprofilms a model of a solution of the containing left of the contains can be covalently attached.	
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pharmaceutically active compounds. After administration, the coupled medicament wil not diffuse from the circulating blood into the interstitum. Clearance by liver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, vasodilation, function of exythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as
                                                                                                                                                                                                                                        1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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                                                                                                                                                           100.0%; Score 4640; DB 8
100.0%; Pred. No. 3e-278;
ive 0; Mismatches 0
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Matches 821;
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The present sequence is the protein sequence of recombinant gelatin-like protein Hu-1 ADM48390. A claimed composition suitable as a substitute for plasma composition suitable as a substitute for plasma composition. The protein is a recombinant gelatin-like protein with a composition. The protein is a recombinant gelatin-like protein with a concular weight of at least 10 kba and at most 50 kba and an isoelectric concular weight of at least 10 kba and at most 50 kba and an isoelectric combinant gelatin-like protein, or a dimer, trimer or tetramer of the protein, is useful as a plasma expander that has a lower clearance rate from blood circulation, provides better and predictable regulation of clearance rate and which is less succeptible to proteolytic degradation than presently used gelatin-like proteins can be covalently attached to pharmaceutically cortive compounds apprehensive. Recombinant gelatin-like proteins can be covalently attached to pharmaceutically cative compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the interstitium. Clearance by cliver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotthing vasodilation, function of cerythney expressed in the events and leukocytes, immune responses, and blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function.
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                                                                                                                                                                                                                                                                                                               Plasma substitute; Gelatin-like protein; plasma expander; human.
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100.0%; Pred. No. 5.1e-207;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                        Human recombinant gelatin-like polypeptide Hu-3.
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                                            AA.
                                     ADM48391 standard; protein; 617
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les 616; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                 03-JUN-2004
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                                                                                                           ADM48391;
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culture support comprises the step of coating a microcarrier bead with gelatine or galatine-like protein having a molecular weight of about 40-
CC 200 kDa, and optionally further comprising the step of immobilising the C gelatine or gelatine-like protein on the microcarrier. In this process, cmore than 75%, preferably more than 85% and more preferably more than 95% of the gelatine or gelatine-like protein has the same molecular weight.
CC of the gelatine or gelatine-like protein has the same molecular weight.
CC of 50.500 um size coated with a gelatine-like protein consists of microbeads of 50.500 um size coated with a gelatine-like protein consisting of at cleast 95% Oly-xaa-vaa triplets and containing at least 15% proline cresidues and less than 5% of hydroxyproline residues, with a molecular weight distribution showing a maximum between 40 and 200 kDa, at least 75% of the protein molecules having a molecular weight within 2% of the maximum. Large-scale production of expressed products can be accomplished with gelatine-coated microcarriers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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Local Similarity 100.0%; Score 3482; DB 8; L
Local Similarity 100.0%; Pred. No. 5.1e-207;
Nes 616; Conservative 0; Mismatches 0;
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                                    GPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is porcine alphal(I) collagen. The present invention relates to recombinant synthesis of collagens and gelatins derived from animals. Collagen is an important component of arterial scalaris, food and cosmetic industries. Collagen is an important component of arterial scalaris, bone grafts, drug delivery system, dermal implants, haemostats, and incontinence implants, and for treating autoimmune disorders such as rheumatoid arthritis. Collagen is useful in food products such as rheumatoid arthritis. Collagen is useful in vaccine formulations for treating viral infections, autoimmune diseases and cancer. Gelatin is useful in the manufacture or as a component of various pharmaccutical and edical devices and products, in food and beverage industries, in hair care and skin care products, as a glue or adhesive in various manufacturing processes, as a light-sensitive coating in various celectronic devices, as a photocoatist base in photolithographic processes, in printing and photographic applications, in laboratory application, and as a light as a light sensitive coating in various as a light and photographic applications, in laboratory application, and as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a light sensitive coating in various as a light as a li
                                                                                                                                   Porcine; alphal(I) collagen; gelatin; cytostatic; viral infection, bharmaceutical; food industry; cosmetic; autoimmune disorder; vaccine; medical; arterial sealant; bone graft; dermal implant; haemostat; cancer; rheumatoid arthritis; beverage; photographic application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                                   839. .830
/note= "Encoded by ggcgaacctggtgatgctggtgctaaaggcgatg
ctggtccccccggccctgctgga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated and purified bovine or porcine collagens and gelatins useful in medical, pharmaceutical, food and cosmetic industries, as vaccine, and for treating autoimmune disorders, infections and cancer.
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56.7%; Pred. No. 1.4e-162;
ive 32; Mismatches 226;
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                                                                            Porcine alphal(I) collagen
                        (first entry)
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N-PSDB; AAD06576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                              Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1999;
                        10-AUG-2001
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The specification describes a method for producing an extracellular matrix protein is matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily capable of self aggregating in a cell which does not ordinarily converses optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-conto the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional contents depends on the post translational hydroxylarion of proline. The proteins depends which do not normally contain trans-4-hydroxyproline. The present sequence represents human collagen 1 (alpha1) helical region, which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                          Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful on medical implants.
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                                                                                                                                                                                                                                                           Connolly
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                                                                                                                                                                                                                                                         Zhang G,
                                                                                                                                     99EP-00119184
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                                                                                                                                                                                                                                                                                                  WPI; 2000-259138/23.
N-PSDB; AAA12503.
                                                                                                                                                                              09-OCT-1998;
                 Homo sapiens
                                                                                                                                       07-OCT-1999;
                                                       EP992586-A2
                                                                                                12-APR-2000
                                                                                                                                                                                                                                                             Gruskin EA,
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Sequence 1057 AA;

19; GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105 150 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 197 GPPGPAGPAGERGEQGP-----AGSPGFOGLPGPA 180 GPRGSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 257 -----GPSGPA-----GEPGPT 213 GLPGPPGERGGPGSRGFPGADGVAGFKGPAGERGSPGPAGFKGSPGEAGRPGEAGLPGAK 273 57 77 18 GPMGPSGPRGLPGPPGAPGPQGPPGEPGASGPWGPRGPPGPPGRNGDDGEAGRP GOAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---Gaps Query Match
59.6%; Score 2765; DB 3; Length 1057;
Best Local Similarity 55.4%; Pred. No. 1.1e-162;
Matches 561; Conservative 31; Mismatches 228; Indels 192; GPPGEAGKPGEQGVPGDLGAP-----28 78 901 138 151 198 181 214 엄성엄 g à g ò qq δ ò

619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 675 735 GXAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA 771 977 393 497 423 558 GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPXGADGSPGXDGVRGLTGPIGPPGPAGAP 617 678 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 737 562 GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618 738 GPAGKEGGKGPKGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGGR 797 437 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 377 GLPGAKGLIGSPGSPGFDGKIGPPGPAGQDGRPGPPGPPGAKGQAGVMGFPGPKGAAGEP GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GEQGVPGDLGAPGPSGPAGE-----PGP-----TGLPGPP 424 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLP 475 GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ------516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGPPGAVGGPPGPKGAAGEPGKAGER GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG 820 798 919 772 274 378 334 394 셤 ò g g ò g δ ద δ g à g ò ò g à ò 셤 δ

Ŕ AAY84403 standard; protein; 1058 (first entry) 12-JUL-2000 AAY84403,

Amino acid sequence of human type 1 (alpha1) collagen polypeptide.

Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bloadhesive. 98US-0099652P 99WO-US020462 WO200014201-A1 09-SEP-1998; 07-SEP-1999; Homo sapiens 16-MAR-2000. AAN 94403
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         ---GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ-----
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Misc-difference
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                                                                                                                                                                                           The present sequence represents a human type 1 (alphal) collagen protein. Peptides derived from the protien were used to demonstrate incorporation in 3.4-debydro---proline into the peptide, using the method of the invention. The specification describes a method for the incorporation of non-natural amino acid into a polypeptide. The method comprises reacting at least one 3.4-debydroproproline residue in the polypeptide with an epoxyproline residue. The method is quad containing at least one 3.4-debydroproline residue. The method is used for studying the effects of non-abtural amino acids on structure and function of polypeptides. The method is also useful for commercial production of collagen or mussel adhesive proteins (which are useful as bloadhesives), and for incorporating a widevariety of groups, including therapeutic ligands and biological probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105
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                                                                                                               e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.6%; Score 2765; DB 3; Length 1058; Best Local Similarity 55.4%; Pred. No. 1.1e-162; Matches 561; Conservative 31; Mismatches 228; Indels 192;
                                                                                                        Incorporating non-natural amino acid into polypeptide, useful production of bloadhesives, by epoxidation or substitution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEQGVPGDLGAPGPSGPAGE------PGP----
                                 Buechter DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPPGEAGKPGEQGVPGDLGAP-----
                                                                                                                                                                  Disclosure; Fig 6; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPPGPAGPAGERGEQGP-
                             Paolella DN, Gruskin EA,
                                                                                                                         production of bioadhesivedehydroproline residues.
                                                             WPI; 2000-271051/23.
 BUECHTER
                                                                                                                                                                                                                                                                                                                                                                                    polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1058 AA;
                                                                           N-PSDB; AAZ99843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; decorin; ohimera.
                                                 GPAGP --- AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                 679 GPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP
                                                                                                                                                                            739 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
                                                                                                    619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                                                799 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP
                                                                                                                                                                                                               736 GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA
                                                                                                                                                                                                                                           919 GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA
                                                                                                                                                          676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a chimeric collagen 1 (alphal)/decorin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                                                                                                                                                                                                                                      GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG 820
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily by droxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell, incorporating the nucleic acid sequence into the cell; and contacting the incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium concaining at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated incorporated from a second to make how cell and incorporated into the extracellular matrix protein. The hydroxyproline into proteins this is especially useful in the recombinant production of proteins such as collagen, fibrinagen and produce functional proteins depends on the post translational hydroxylation of proteins depends on the post translational hydroxylation of proteins which do not normally contain trans-4-hydroxyproline. The present sequence represents a chimeric collagen I (alphal)/decorin to protein, which may be produced using the method of the invention

Sequence 1107 AA;

19; GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105 150 180 257 213 317 273 333 GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393 GEQGVPGDLGAPGPSGPAGE-----PGP-----TGLPGPP 423 557 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLP 474 617 137 57 77 -----AGVMGFPGPKGAAGEPGKAGBRGVPGPPGA------VGPAGKDGEAGAQGPP GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPXGADGSPGKDGVRGLTGPLGPPGPAGAP 214 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GEOGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP GAK------GLTGSPGPDGKTGPPGPAGDDGRPGPPGARGQ-----GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---18 GPMGPSGPRGLPGPPGAPGPQGPQGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKP 106 GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ ------BGSPGFOGLPGPA 198 GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS GPPGEAGKPGEQGVPGDLGAP------GEPGPT GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER Gaps 59.6%; Score 2765; DB 3; Length 1107; 55.4%; Pred. No. 1.2e-162; iive 31; Mismatches 228; Indels 192; GPPGPAGPAGERGEQGP Query Match Best Local Similarity 55.4% Matches 561; Conservative 558 475 151 181 258 318 274 378 334 438 394 498 424 618 516 58 음성음 2 8 2 g 6 B 6 B 6 ద à g à dd δ 셤 ઠે g ò ò

Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. transforming growth factor-betal; TGF-betal; chimera. 618 675 GKAGERGVPGPPGAVGPAGKDGE------AGAQGPPGP------AGPA 771 918 GPAGARGPAGPPGDRGTGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGPGGPSGASGPA 977 The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; ö 676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 138 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR 619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful medical implants. GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1029 GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG A chimeric collagen 1 (alpha1)/TGF-betal protein. ਨ. Connolly /note= "Gly encoded by GCT' Ö Ź Location/Qualifiers Claim 23; Fig 15; 260pp; English. Zhang AAY84538 standard; protein; 1171 99EP-00119184. 98US-00169768. (first entry) Buechter DD, (USSU) US SURGICAL CORP. WPI; 2000-259138/23. N-PSDB; AAA12498 Key Misc-difference 09-OCT-1998; 25-JUL-2000 Homo sapiens Unidentified Gruskin EA, 12-APR-2000 EP992586-A2 AAY84538; 736 772 978 Chimeric 562 AAY84538 g g g ò 셤 à ò $\dot{\delta}$ ò

GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGPVGPAGKSGDRGETGPAGPAGPV GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP

-----AGAOGPPGP------AGPA

GKAGERGVPGPPGAVGPAGKDGE--

GPAGARGPAGPQGPRGDKGTKGHRGF8GLQGPPGPPGSPGEQGPSGASGPA

임 8

AAW68485 standard; protein; 1464 AA.

Human recombinant collagen protein.

(first entry)

08-DEC-1998

AAW68485;

GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG

GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 675 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP 857

619 198 9/9 828 736 918 772

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incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-6 hydroxyproline and allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of postpeptides which do not normally contain trans-4-hydroxyproline. The present sequence represents chimeric collagen 1 (alphal)/transforming growth factor-betal (TGF-betal) protein, which may be produced using the method of the invention
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; Pred. No. 1.2e-162;
31; Mismatches 228;
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Primer; PCR; amplification; human; collagen; mammal; plant; prosthesis; cardiac valve; ligament; tendon; skin; gingival implant; perfumes; nerve regeneration; antibiotic; growth factor; cancer; inflammatory; gelatin; glue; food Merot B; "cleavage site for carboxypeptidase" Garrone R, 'note= "cleavage site for aminopeptidase" Comte J, "signal peptide" "mature protein" Ľ Location/Qualifiers Ruggiero 97WO-FR002331. 96FR-00016224. .999 'note= Exposito J, /note= note= WPI; 1998-362771/31. (BIOC-) BIOCEM SA. N-PSDB; AAV60814. Cleavage-site Cleavage-site Homo sapiens. WO9827202-A1 17-DEC-1997; 17-DEC-1996; 35-JUN-1998. Gruber V, Bournat P; Synthetic Peptide Protein AAW68485
AAW6
AAW6
AAW6
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AAW6
CXX
KW Carc
K

Disclosure; Fig 7; 138pp; French.

in and

New recombinant nucleic acid for expressing collagen or derivatives plants - useful as, e.g. blo-materials and in therapeutic, cosmetic

plants - useful as, e.g. bi odontological compositions.

677 561 678 GPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 737

q

516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP

GAK------GLTGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ--

558

g

424

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475

à qq ò 562 GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618

498 ĠEĠĠVPĠDĽĠAPĠPŚĠARĠĖRGPPGERGVQGPPĠPAGPRGANGAPGNDGAKGDAĠAPĠAP 557

GEQGVPGDLGAPGPSGPAGE------PGP-

394

ò g GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE------AGRPGEAGLP GSQGAPGLQGMPGERGAAGLPGPKGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP

474 617 515

----TGLPGPP 423

The invention relates to the production of mammalian collagen in plants. 2 clones: alpha3 and alpha22, spanning the human collagen type I gene were isolated from a MG-63 osteosarcoma library. Clone alpha3 contained 83 bp of the 5' untranslated region and the first 1920 bp of coding sequence, whereas clone alpha22 contained sequence encoding amino acids

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The 2 clones were used to generate a number of fragments which were used to generate a number of fragments which were used to generate a number of fragments which were used to construct composite sequences encoding variant collagen molecules. The fragments are: (A) containing nucleotides (nt) '-4 to 479; (B) containing the protein and bases (6-77 from the sequence encoding the corrections of the pro-collagen amino propeptide domain; (C) the whole of the amino propeptide domain (nt 7-479); (D) all of the amino-telopeptide domain (nt 7-479); (D) all of the amino-telopeptide domain (nt 474-534) and the N-terminus of the helicoidal region (nt 535-57-356 of the central helicoidal domain; (F) the BamHI-EcoRI (2803-4362) region of alpha22, encoding as 356-192 in the central helicoidal domain (c) treps of all 193-1454 in the C-propeptide domain; (G) the C-terminus of the C-propeptide domain (as 1346-1464) plus stop codors, and (H) as G but concing as 1349-1401 and also including the KDES motif for referring from the ER. This sequence represents a recombinant human collagen. The encoding gene was constructed from fragments (A), (D), (E), (F) and (G). The recombinant gene is used for expression of mammalian collagen. The plant cells. The transformed plants, their extracts and parts are useful compositions (e.g. as prosthesesses sponges or bandages) and in pharmaceutical, medical, odontological, cosmetic and biotechnological compositions (e.g. as prostheses for cardiac valves, ligaments or tendons; skin substitutes; gingival implants; microcapsules for partial surgical thread and components of ointments). They are suitable for treating any disorder related to collagen dysfunction and gelatin, produced from collagen, is urgical prostheses and foods 8888888888888888888888888888888888

Sequence 1464 AA;

19; 238 105 298 150 299 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 358 180 359 GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGOPGAKGANGAPGIAGAPGFPGARGPS 418 GPPGEAGKPGEQGVPGDLGAP-----GEPGPT 213 478 GLEGEPGERGGERGFFGADGVAGFKGFAGERGSFGFAGFKGSFGEAGREGEAGLFGAK 273 538 333 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 598 GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393 GEOGVPGDLGAPGPSGPAGE-----PGP-----TGLPGPP 423 deggivegolidabgessandergergergvogeredergergangargndakgdadareare GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLP 474 58 GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR GQAGVMGFPGPKGAAGEPGKAGER----GVPGPPGAVGPA-----GKDGEAGAQ ----AGSPGFOGLPGPA GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---Gaps Query Match 59.6%; Score 2765; DB 2; Length 1464; Best Local Similarity 55.4%; Pred. No. 1.5e-162; Matches 561; Conservative 31; Mismatches 228; Indels 192; GPPGPAGPAGERGEOGP 239 106 151 181 419 214 479 274 539 334 599 394 559 124 g g ò a ò g 상 원 ò ò ò ઠે g ò g ठे 8

.079 GPAGARGPAGPRGDRGETGEQGDRGIKGHRGFSGLQGPFGPPGSPGEQGPSGASGPA 1138 959 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP 1018 The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also GPTGLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 675 839 GPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 898 618 899 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR 958 for GPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEP GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal. GAK------GLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGARGQ------516 ----AGVMGFPGPKGAAGBPGKAGBRGVPGPPGA------VGPAGKDGEAGAQGPP Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. GERGEOGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPAG Σ Costigan Human Protein P02452, SEQ ID NO 10491. Ä ADD45059 standard; protein; 1464 Claim 1; Page; 1017pp; English. Befort K, 14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P. 14-AUG-2002; 2002WO-US025765 (first entry) (GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG. Woolf C, D'urso D, WPI; 2003-268312/26. GENBANK; P02452. WO2003016475-A2 Homo sapiens 29-JAN-2004 27-FEB-2003 619 ADD45059; 295 736 772 719 RESULT 10 ADD45059 g 8 셤 ò 유 D D ò 셤 ò ద ò ò 9 . 8

RESULT 11 ADD45055 g ò ద 8 유 ò g 셤 à g 8 claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a creases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence ct that increases or decreases the expression of the polynucleotide sequence ct expression of a polynucleotide sequence which is differentially amethod for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the cutoffication, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the compound apparamental composition compression or more of pain and a pharmaceutical composition comprising the one or more compound useful in treating computation and spared nerve injury (CMung), chronic constriction contraction contraction contraction contraction contraction contraction contraction which is edifferentially expressed during pain. Note: The sequence data for this patent did not form part of the printed contraction in the sequence data for this patent did not form part of the printed contraction in the sequence data for this patent did not form part of the printed contraction in the sequence data for the sequence form of the printed contraction in the sequence data for this patent did not form part of the printed contraction in the sequence data for this patent did not form part of the printed contraction in the sequence data for the sequence form of the printed contraction in the sequence data for this patent did not form part of the printed contraction in the sequence data for the sequence form of the printed contraction in the sequence data for the sequence data for the sequence data for the sequence data for the sequenc 179 GPMGPSGPRGLPGPPGAPGPQGPQGPGEPGBPGASGPMGPRGPPGPPGKNGDDGEAGKP 238 GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105 213 4.78 ĠQMĠPRĠLPĠERĠRPĠAPĠPAĠARGNDGATĠAAĠPPĠPTĠPAGPPGFPGAVĠAKĠEĀĠPQ 358 -AGSPGFQGLPGPA 180 GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 418 333 GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393 658 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA--- 57 ----TGLPGPP 423 GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP 718 GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ------515 GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPAGFAGKP GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ --GPSGPA-----GEPGPT GPOGPPGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPT GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GLTGSPGSPGRDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER Length 1464; GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE----GEQGVPGDLGAPGPSGPAGE------PGP-----59.6%; Score 2765; DB 7; 55.4%; Pred. No. 1.5e-162; iive 31; Mismatches 228; specification, but was obtained in electr
ftp.wipo.int/pub/published_pct_sequences. GPPGPAGERGEOGP------= = = = Query Match Best Local Similarity 55.49 Matches 561, Conservative Sequence 1464 AA; 214 28 106 151 359 181 419 479 274 99 334 394 629 \$24 719 475 g à g ò БЪ ò g ò 셤 ò Db ò g ö d g ò ò

1019 GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPV 1078 GPAGARGPAGPQGPRGDKGETGEQGDRGIXGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 1138 958 735 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 675 779 GDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDA 838 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG 820 736 GKAGERGVPGPPGAVGPAGKDGE-----562 899 619 919 772

ADD45055 standard; protein; 1464 AA.

ADD45055;

Human Protein P02452, SEQ ID NO 10487.

pain; neuronal tissue; gene therapy; segmental nerve injury; chronic constriction injury; CCI; nerve injury; SNI; Chung. spared spinal

Homo sapiens.

WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

(GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.

Costigan M; Befort K, Woolf C, D'urso D,

2003-268312/26. GENBANK; P02452 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent

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that increases or decreases the expression of the polynucleotide sequence that increases or decreases din neutonal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed segmence data for this patent did not form part of the printed segmental and an animal (e.g. specification) but was obtained in electronic form directly from WIPO at the printed segmental and the presented or the printed segmental and the printed segmental and the printed segmental and the presented or the printed segmental and the printed segmental and the printed segmental and the printed segmental se
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Sequence 1464 AA;

418 598 393 658 423 718 538 333 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP 561 213 478 273 179 GPMGPSGPRGLPGPPGAPGPQGPQGPPGEPGRSGPMGPRGPPGPPGKNGDDGEAGKP 238 105 GOAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ 150 -----AGSPGFQGLPGPA 180 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 358 479 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 359 GPRGSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 214 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 539 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GVPGPPGAVGPAGKDGEAGAQGPPGPAGFAGFAGFAGFAGSPGFQGLPGPAGFPGEAGKP GEQGVPGDLGAPGPSGPAGE------PGP-----PGP-----TGLPGPP GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE------AGRPGEAGLP GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---GPPGEAGKPGEQGVPGDLGAP-----GEPGPA-----GEPGPA GAK------GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ------59.6%; Score 2765; DB 7; Length 1464; 55.4%; Pred. No. 1.5e-162; ive 31; Mismatches 228; Indels 192; Gaps GPPGPAGPAGERGEQGP--------Matches 561; Conservative Similarity 274 334 599 394 629 424 719 475 516 28 239 106 299 151 181 Query Match Local дg g à g δ 음 8 d ò 유 ò g ò ò 8 g ò ద ઠે d

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, delarivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increasingly expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially 959 ĠVVĠĹPĠQRĠERĠFPĠLPĠPSĠEPĠKQGPSĠASGERĠPPGPMGPPGLAĠPPĠESGREGAP 1018 1079 GPAGARGPAGPOGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 1138 for GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGTAGQR 619 GPTGLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 736 GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal. 839 GPPGPAGPPGPIĞNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP GPAGP - - - AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP 1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1190 GERGEDGFAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820 Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. Costigan M; Human Protein P02452, SEQ ID NO 10483. ADD45051 standard; protein; 1464 AA. Claim 1; Page; 1017pp; English. Befort K, 14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P. 14-AUG-2002; 2002WO-US025765 (GEHO) GEN HOSPITAL CORP. (PARB) BAYER AG. (first entry) Woolf C, D'urso D, WPI; 2003-268312/26. GENBANK; P02452. WC2003016475-A2. Homo sapiens 29-JAN-2004 27-FEB-2003. ADD45051; 772 899 562 ADD4505 g 용 g 8 ઠે g ò 셤 ઠ ઠે

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expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the particledides, an ethod for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more obypeptides or their artibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CIN) and spared nerve injury (CIN) in a animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GPPGBPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                            59.6%; Score 2765; DB 7; Length 1464;
55.4%; Pred. No. 1.5e-162;
ive 31; Mismatches 228; Indels 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPGPAGPAGERGEOGP
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                                                                                                                                                                                                                                                                                                                          Sequence 1464 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stimulating or inhibiting cell growth and/or division, useful for stimulating chondrogenesis, cartilage, disc or connective tissue growth, repair, and/or regeneration, comprises administering deer antler cartilage gene.
399 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
                                                                                                                                                    1079 GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGESGGSGGPA
                                                GVVGLPGORGERGFPGLPGPSGEPGKOGPSGASGERGPPGPMGPPGLAGPPGESGREGAP
                                                                                                                               ---AGPA
                        619 GPIGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                           GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                                                                                                                                                                     Human; deer; rat; mouse; DACC; deer antler cartilage cell; cell stimulation; cell inhibition; cell growth; cell division; mesenchymal cell; chondrocytei, chondrogenesis; osteogenesis; growth; repair; regeneration; restoration; extracellular matrix; cartilaginous matrix; cartilage; disc; connective tissue; agonist;
                                                                                                                                                                                                    1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPG 1190
                                                                                                                                                                              GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
                                                                                                                             --- AGAQGPPGP-
                                                                                                                                                                                                                                                                                                                                              Human polypeptide orthologous to DACC-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 154-160; 214pp; English.
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                                                                                                                            GKAGERGVPGPPGAVGPAGKDGE--
                                                                                                                                                                                                                                                                   ABG93947 standard; protein; 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-2002; 2002WO-AU000163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-FEB-2001; 2001AU-00003116.
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ADPP-) ADP PHARM PTY LTD. (UNSY ) UNIV SYDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonist; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-643456/69.
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                                                                                                                                                                                                                                                                                                                     26-NOV-2002
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The invention discloses a method for stimulating or inhibiting cell growth and/or division which comprises contacting or inserting into an animal cell a polypeptide comprising one of the deer antler cartilage cell (DACC) clones disclosed. More particularly, the method relates to these polypeptides stimulating mesenchymal cell growth and/or division and to transfecting these cells and chondrocytes with vectors carrying the genes of these polypeptides capable of stimulating chondrogenesis, osteogenesis, growth, repair, regeneration and/or restoration of the extracellular matrix. The chondrocytes selectively express genes required to form a cartilaginous matrix. The DACC polypeptides and polymodeotides are useful for identifying an agent that modulates the activity of the polypeptide, for stimulating mesenchymal cell growth and/or division by exposing animal mesenchymal cells to conditioned media or its active

growth and/or division by inserting into an animal cell, a compound which inhibits the translation of the polymuclectide encoding the DACC. The method and the polymethes are useful for stimulating mesenchymal cell growth and/or division or for stimulating chondrogenesis, cartilage, or connective tissue growth, repair, regeneration and/or restoration in an animal. The polymuclectides, polymethes, agonists and antagonists may be used in treatment modalities, specifically in gene therapy. The polymetide can be used as bait proteins in a two- or three-hybrid assay to identify other proteins, which bind to or interact with the polypeptide and are involved in modulating cell growth and/or division. The sequences presented in ABG93923-ABG93948 are the proteins encoded by the DACC cDNA clones

Sequence 1461 AA;

775 515 561 895 618 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 675 715 474 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR 955 393 655 423 415 213 273 535 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 333 595 235 105 GRPGERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAP 295 GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ 150 ----AGSPGFQGLPGPA 180 836 GPPGPAGPAGPPGPIGNVGAPGAKGAKGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 596 GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 656 GEĞGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE------AGRPGEAGLP GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ----------AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP GPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GPMGPSGPRGLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPRGPPGPPGRAGDDGEAGKP 296 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 356 GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGOPGAKGANGAPGIAGAPGFPGARGPS ----TGLPGPP 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR Length 1461; Indels GEQGVPGDLGAPGPSGPAGE-------PGP-----Score 2761; DB 5; Pred. No. 2.6e-162; 1; Mismatches 229; GPPGPAGPAGERGEQGP------31; GPPGEAGKPGEQGVPGDLGAP-59.5%; Conservative Similarity Matches 560; 424 516 716 475 295 236 181 416 214 476 274 536 334 394 9/1 28 151 106 Local g g Dp δ g ò g ò 셤 ò ò 쉽 ò g à ò 셤 d d ò 엄 8 ò à 셤 ò

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the invention relates to polymucleotides encoding novel human proteins or their active domains. The polymeptides, polymucleotides and antibodies caused against the polymeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polymeptides can be used as molecular weight markers, food supplements, and in antibody production. The polymeptides care used to identify compounds which bind to the polymeptides.

Polymucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polymeptides of the invention can be used to target drugs to a title as a tissue markers, and to isolate receptors or ligands.

Delympetides of the invention may also be useful in treating platelet disorders, stem cell disorders, seem cell disorders, seem cell disorders, wound healing, treating burns, promoting 1075 devdakdepadepadekderdegobraikgergikaersalaadepedepegepsaasaea 1135 771 immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antival; attibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder. 1016 GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGAPGPVGPAGKSGDRGETGPAGPPV GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP diseases, Isolated polypeptides useful for treating anti-inflammatory diseas nervous system disorders, and for regenerating bone and cartilage protein; Antianaemic; osteopathic; antiinflammatory; GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG -----AGAOGPPGP. Example 4; Page 525-527; 894pp; English. GKAGERGVPGPPGAVGPAGKDGE----Ä AAU14136 standard; protein; 1464 25-JAN-2001; 2001WO-US002623. RT, 25-JAN-2000; 2000US-00491404 entry) Drmanac Human novel protein #7. 2001-451939/48. (first (HYSE-) HYSEQ INC. rang YT, Liu C, N-PSDB; AAS22441 WO200155437-A2 Homo sapiens. 02-AUG-2001. 24-OCT-2001 1076 1136 AAU14136; 772 926 919 736 ò g ઠે 9 ò

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the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fingal infection or from autoimmunity, cancer, allergy, asthma, graftversus-host diseases, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention
                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                    GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105
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                                                                                                                                                                                                                                                                                                  GPMGPSGPRGLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKP 238
                                                                                                                                                                                                                                                                                                                                                                                                              150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPQGPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPT 478
                                                                                                                                                                                                                                                                                                                                                                   GRPGERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGARGDAGPAGPKGBPGSPGENGAP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                           GOMOPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPRGSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      928
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                                                                                                                                                                                                                                                                                                                                                                                                          GQAGVMGFPGPKGAAGEPGKAGER----GVPGPPGAVGPA------GKDGEAGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGBAGRPGEAGLDPGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVPGPPGAVGPAGXDGEAGAQGPPGPAGPAGBRGEQGPAGSPGFQGLPGPAGPAGPPGBAGKP
                                                                                                                                                                                                                                                                 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GPSGPA---~--GEPGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TGLPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGWGFPGPKGAAGEPGKAGER
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                                                                                                                                                                                                                                Indels 192;
                                                                                                                                                                                                  Length 1464;
                                                                                                                                                                                            Query Match 59.5%; Score 2761; DB 4; Best Local Similarity 55.3%; Pred. No. 2.6e-162; Matches 560; Conservative 31; Mismatches 229;
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily dydoxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-slow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-incorporate trans-4-incorporate into the cell and incorporated such as sollagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional contains dependent on the post translational hydroxylation of proteins.
                                                                                  1138
.019 GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGPVGPAGKSGDRGETGPAGPV 1078
                                            771
                                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           method is also useful in studying the structure and function of polypeptides which do not normally contain trans-4-hydroxyproline. The present sequence represents a human collagen 1 (alpha1) protein, which may be produced using the method of the invention
                                              --AGPA
                                                                                GPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                                                                                                1139 GPRGPPGSAGAPGXDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1190
                                                                                                                          820
                                                                                                                    772 GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a human collagen 1 (alpha1) protein.
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Pred. No. 2.7e-162;
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                                          GKAGERGVPGPPGAVGPAGKDGE
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Best Local Similarity
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GPAGP---AGERGEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGEP 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738 GPACKEGCKGPRGETGPACRPCEVGPPGPPGPACEKGSPCADGPACAPGTPCPCGIACOR 797
 19;
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                                              181 GPPGEAGKPGEOGVPGDLGAP----GEPGPT
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560; Conservative 31; Mismatches 229; Indels 192; Gaps
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Sequence 1, Ap
Sequence 18, A
Sequence 18, A
Sequence 18, A
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- 2004 Compugen Ltd.
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US-09-548-608-18

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US-08-941-820-3

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                                                                                                           October 18,
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US-09-331-347C-21

Sequence 21, Application US/09331347C

Sequence 21, Application US/09331347C

Sequence 21, Application US/09331347C

Sequence 21, Application US/09331347C

Sequence 21, Application:

APPLICANT: Meristem Therapeutics, S.A.

APPLICANT: Meristem Therapeutics, S.A.

TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, h

TITLE OF INVENTION: obtaining Such and Their Uses

TITLE OF INVENTION: 050431,347C

CURRENT FILING DATE: 1999-08-17

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.1

SEQ ID NO 21

LENGTH: 1464
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ilarity 55.4%; Pred. No. 2.9e-171;
Conservative 31; Mismatches 228; Indels 192;
US-09-548-608-19
US-09-588-887-10
US-09-589-578-10
US-08-642-205-2
US-08-642-205-53
US-09-219-449-5
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         TYPE: PRT ORGANISM: Homo sapiens
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62, Appli 20, Appli 20, Appli 20, Appli 20, Appli 20, Appli 12, Appli 4, Appli

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                                                                       GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGPR
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  Gaps
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  Conservative
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Sequence 9, Application US/0958587;
Sequence 9, Application US/0958587;
GENERAL INFORMATION:
APPLICANT: Olsen, David R
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chandlin, Hugh
APPLICANT: Chisholm George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/585,887
CURRENT APPLICATION NUMBER: US/09/289,578
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTH OF ILIANT OF IL
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                                                                              619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER
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                                           GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
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Pred. No. 2e-170;
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US-09-585-887-9
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Best Local Similarity
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US-09-585-887-9
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                                                                                     GPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                                                                                                                                                                                 676 GLEGAKGLIGSPGSPGPDGKIGPPGPAGDDGRPGPPGPPGARGOAGVMGFPGPKGAAGEP
                                                                                                                                              896 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
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Sequence 1, Application US/08931820
Sequence 1, Collo663
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Assay for collagen
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFFRATING SYSTEM: PC-DOS/NS-DOS
OFTWARE: Patentin Release #1.0, Ver;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
CLASSIFICATION 0435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
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Collagen type I
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
TYPE: amino acid
STRANDEDNESS: single
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GENERAL INCRWATION:
APPLICANT: Chang Robert
APPLICANT: McMullin, Hugh
APPLICANT: McMullin, Hugh
APPLICANT: McMullin, Hugh
ITILE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
ITILE OF INVENTION: PULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
ITILE OF INVENTION: CELLA
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55.2%; Pred. No. 2e-170;
ive 31; Mismatches 230; Indels 192
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              Sequence 9, Application US/09289578
Patent No. 6428978
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Best Local Similarity 55.23
Matches 559; Conservative
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US-09-289-578-9
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                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          DATA:
: US/08/963,825
                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFREENCE/DOCKET NUMBER: 4306
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-27-7700
TELEFAX: 212-753-6237
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CLONE: COLLAGEN ALPHA 1 (I)
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TELEX: 236687
INFORMATION FOR ED ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
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New York
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Matches 542; Conserv
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Length 1341;

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480

430 GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLPGAK--- 477

TGLPGPPGERGGP

us-10-658-989a-3.rai

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                                                                                                                                                                           Query Match 58.3%; Score 2704; DB 3; Best Local.Similarity 57.3%; Pred. No. 2.3e-167; Matches 542; Conservative 28; Mismatches 244;
                                                                                                                                                                                                                                                   1 GPPGE---PGPTGLPGPPGERGGPGSRGF-
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                                                                                                  INMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1
US-09-500-811-18
                                                                                       ORGANISM: Homo sapiens
                                                     protein
                 TYPE: amino acid TOPOLOGY: linear
                                                 MOLECULE TYPE: ORIGINAL SOURCE:
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Sequence 18, Application US/09500811

Sequence 18, Application US/09500811

APPLICANT: Ovist, Per APPLICANT: Ovist, Per APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the TITLE OF INVENTION: Disorders Associated with the Method to Disgnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS: 21

CORRESPONDENCE ADDRESS: 4

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CONTRANT OF PARTICIAL OF APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT: IRFORMATION:
NAME: GOODIE AAAA
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REGISTRATION NUMBER: 29,714
REPRENCE/DOCKET NUMBER: 4305,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEKAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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US-09-500-811-18
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GERGEQGPAGSPGFPGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPP 219
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US-09-548-608-18

US-09-548-608-18

Sequence 18, Application US/09548608

Patent No. 6355442

GENERAL INFORMATION:
APPLICANT: Orist, Per
APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carry
TITLE OF INVENTION: Method and Use of the Method to Diagnose the F

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                                                                                                                                                                                                           Sequence 18, Application US/09570573

Patent No. 6342361

GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 GPPGRDGIPGQPGLPGPPGPPGPPGLGGNFAPQLYGYDEKSTGGISVPGPMGPSGPR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPGARGQAGVMGFPGPXGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGA 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42
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llarity 57.3%; Pred. No. 2.38-167;
Conservative 28; Mismatches 244; Indels 132
                               ---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                             ZIF: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPPGE---PGPTGLPGPPGERGGPGSRGF-
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/
TELECOMMUNICATION INFORMATION:
TELERAN: 212-527-7700
TELERAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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Best Local Similarity
Matches 542; Conserv
                               GPAGSP-
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                                                                                                                                                                                          US-09-570-573-18
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Sequence 49, Application US/09219849

Fatent No. 615081

GENERAL INFORMATION:
APPLICANT: VAN NIEDS.
APPLICANT: VAN NIEDS.
APPLICANT: WAN RIDNA ALEXIS C.
APPLICANT: BOUNGTRA, JAN S.
APPLICANT: BOUNGTRA, JAN S.
APPLICANT: WOORDOOK, ANDREAS.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND RICHELE D.
APPLICANT: WIND SOCH, TANJA J.
APPLICANT: WIND SOCH, TANJA J.
APPLICANT: WIND SITTLE D.
APPLICANT: WIND SOCH, TANJA J.
APPLICANT: WIND SOCH, TANJA J.
APPLICANT: WIND REPRANTION SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
CURRENT FILING DATE: 1998-12-23
SOCTWARE: PATENTIN VET: 2.1
SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            961 GPAGPOGPRGDKGETGEOGDRGIKGHRGFSGLOGPPGPPGSPGEOGPSGASGPAGPRGPP 1020
         661 GPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDAGPPGPA 720
                                                                                                                     721 GPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPAGKE 780
                                                                                                                                                                                                                                          781 GGKGPRGETGPAGRPGEVGPPGPPGPPGBKGSPGADGPAGAPGTPGPQGIAGQVGUPPGPP
                                                                                                                                                                                                                                                                                                 625 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEAGLPGAK 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPPGBPGPTGLPGPPGB------RGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 GSAGAPGKDGINGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPG 1066
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                                                                      GVMGFPGPKGAAGEPGKAGERGVPGPPGA-
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 GNSGE-----PGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLPGPP 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDLGAPGPSGPAGE-----PGP----PGP----TGLPGPPGERGGP 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 GDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQGAP 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 GLÞGÞPGAPGPZGFZGPPGZPGASGPMGPRGPPGPPGKBGBBGZAGKPGRÞGZRGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 GAVGPAGKDGEAGAQGPPGPAGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/187,319
FILING APPLICATION NUMBER: 08/187,319
FILING APPLICATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEERA: 212-753-6237
TELEBRAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.3%; Score 2704; DB 3; Best Local Similarity 57.3%; Pred. No. 2.3e-167; Matches 542; Conservative 28; Mismatches 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPPGE---PGPTGLPGPPGERGGPGSRGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (1)
US-09-548-608-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: ami
TOPOLOGY:
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PRIOR APPLICATION NUMBER: US 07/487,732 PRIOR FILING DATE: 1990-03-02 PRIOR FILING DATE: 1990-03-02 PRIOR FILING DATE: 1990-07-10 PRIOR FILING DATE: 1990-07-10 PRIOR PELLOR TOWNER: US 07/379,778 PRIOR FILING DATE: 1999-07-14 PRIOR PELLOR NUMBER: US 07/607,826 PRIOR PELLOR NUMBER: US 07/607,826 PRIOR PELLOR NUMBER: US 07/607,826 PRIOR APPLICATION NUMBER: US 07/695,468 PRIOR PELLOR DATE: 1990-10-10 PRIOR PELLOR DATE: 1990-10-10 NUMBER OF SEQ 1D NOS: 13 SOFTWARE: PATENTING DATE: 1901-10 SEQ 1D NO 10 LENGTH: 1017 TYPE: PRT TYPE: PRT TYPE: PRT	Query Match Query Match Best Local S Matches 506 Y b 25 Y 61 Y 91	145 GNDGOPGPAGPPGPAGGPGPAGGPGRAGBAGPTGARGPEGAQGPRGEPGTPGSPGPA 142GKDGEAGAQGPPGPAGBAGERGEQGPAGSPGFGGAQGPRGEPGTPGSPGPA 150 GASGNPGTDG1PGAKGSAGPGTAGAPGFPGAGPTGPAGPPGBAGKPGBGGVP 156 GD	185
148 GAGGPPGPAGENGEGGPAGSPGFQLEGBAGPPGEAGKPGEQ 192	432 GROGEAGAGGERGERGERGERGERGERGERGERGERGERGERGERGER	580 GFGGLPGPAGEPGEACKPGEQGVPGDLGAPGEPSGPAGEPGPTGLPGPPGERGGP 633 GFAGPPGANGCPGAKGEPGDTGVKGDAGPPGPAGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP	RESULT 10 US-08-468-996-10 US-08-468-996-10 Sequence 10, Application US/08468996 Sequence 10, Application US/08468996 Sequence 10, Application US/08468996 Sequence 10, Application US/08468996 Sequence 10, Application APPLICANT: Miller, Howard APPLICANT: Aimel APPLICANT: OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION TITLE OF INVENTION: GLUCAGON TITLE OF INVENTION: GLUCAGON FILE REPERMOR: 109/0899-00-07 PRIOR APPLICATION NUMBER: US 07/460,852 PRIOR PELING DATE: 1990-10-15 PRIOR PELING DATE: 1990-10-15 PRIOR APPLICATION NUMBER: US 07/065,734 PRIOR APPLICATION NUMBER: US 07/454,486 PRIOR PELING DATE: 1989-12-20

GAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGP----PGPAGPAGERGE-

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us-10-658-989a-3.rai

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640 GDPGPPGARGPPGSRGDPGPPGAPGPPGSRGDPGPPGAPGPPGAPGPPGSRGDPGPP 699
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     160 GAPGPAGPPGSKGDPGPPGAPGPAGPPGSRGDPGPPGAPGPPGSRGDPGPPGPPG 219
                                                                              220 GPPGSRGDPGPPGAPGPPGSRGDPGPPGAPGPAGPPGSRGDPGPPGAHGPAGPKGAH 279
                                                                                                                   226 GSRGFPGADGVAGPK---GPAGERGSPGPAGPKGS---PGEAGRPGEAGLPGAKGLTGSP 279
                                                                                                                                            280 GS------PGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP 327
                                                                                                                                                                                                                              340 GAPGPAGPPGSRGDPGPPGAPGPAGPPGSRGDPGPPGAPGPAGPPGSRGDPGPPGAPGPA 399
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                                                169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGP---AGEPGPTGLPGPPGERGGP
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TITLE OF INVENTION: Assay for collagen degradation
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EP
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
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                   735
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--KGLT
                                                                                                       GAPGAPGPPGSPGPAGPTGKQGDRGEAGAQGPMGPSGPAGARGIQGPQGPRGDKGEAGEP
                                                                                                                                            GK---AGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
                                                                    -----AGODGRPGPPGARGOAGVMGFPGPKGAAGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Weight Collagen-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 9411-4187
COMPUTER READABLE FORM:
MEDTING TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTY PC-DOS/MS-DOS
SOFTWARE: PATENTY Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FLING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.4%; Score 2478; DB 1;
53.8%; Pred. No. 7.5e-153;
ive 33; Mismatches 281;
GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA
                                                                                                                                                                                                                                                        GPPGPRGRSGETGPAGPPGNPGPPGPPG 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Sequence 62, Application US/08642255
; Patent No. 5773349;
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weig;
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
                                                                                                                                                                                                                     GPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPANE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1064 amino acids
                                                                      GSPGSPGPDGKTGPPGP
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Best Local Similarity 53.8
Matches 506; Conservative
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CITY: San Francisco
STATE: California
COUNTRY: USA
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STRANDEDNESS: single
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MOLECULE TYPE: protein
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US-08-642-255-62
                                   805
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Sequence 20, Application US/08963825
Patent No. 6110689
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Ovist, Per
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     736 GK---AGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 792
                              824 GOOGAPGASGDRGPPGPVGPPGLTGPAGEPGREGSPGADGPPGRDGAAGVKGDRGETGAV
                                                                                   -----AGODGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                                      884 GAPGAPGPPGSPGPAGPTGKQGDRGEAGAQGPMGPSGPAGARGIQGPQGPRGDKGEAGEP
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          GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA
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29,714
205/08701
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 105/08/187,319
FILING DATE: 21-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GGGOTS, Adda C
RESISTANION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
TELECHONE: 212-527-7700
TELECHONE: 212-527-7700
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WIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
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TELEX: 23689
INPORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Darby & Darby 8 Bos Third Avenue New York
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                                                                                   685 GSPGSPGPDGKTGPPGP-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 503; Conserva
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STREET: 80
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TOPOLOGY:
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US-08-963-825-20
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                                                                                                                                                                                                                                                                                                                                  53.4%; Score 2476; DB 3; Length 1060; 50.9%; Pred. No. 1e-152; Live 45; Mismatches 272; Indels 168
                                                                                                                                                                                                                                                                                                                                                    ie-152;
hes 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GEAGLPGAKGLTGSP---GSPGP-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
FILLING DATE:
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                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Collagen type II
                                                                           INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity
Matches 503; Conserv
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17; 53.4%; Score 2476; DB 3; Length 1418; 50.9%; Pred. No. 1.3e-152; tive 45; Mismatches 272; Indels 168;

ndels 168; Gaps 17; -----DGKTGPPGPA--- 90 |:||| | | | GLPGERGRTGPAGARAR 275 SKAGERGVPGPPGAVGPA 141 238 GPKGPAGERGSPGPAGPKGSPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 297 | ||| | :| || | | | GPPGPQGARGFPGTPGLP 215 SPGPAGPKGSPGEAGRP lgth 1418;

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216 GVKGHRGYPGLDGAKGEAGAPGVKGESGSPGENGSPGPMGPRGLPGERGRTGPAGAAGAR 275
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50.9%; Pred. No. 1.3e-152;
ive 45; Mismatches 272; Indels
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GGGGT18, Adda C.
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELERAK: 212-527-7700
TELERAK: 212-527-7700
TELERAK: 212-537
TELEX: 216697
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
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Matches 503; Conservative
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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of
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APPLICANT: Done, Martin
TITLE OF INVENTION: Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1056 GERGLKGHRGFTGLOGLPGPPGPSGDOGASGPAGPSGPRGPPGPVGPSGKDGAMGIPGPI 1115
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                                                              GRPGPPGPQGARGQPGVMGFPGPKGANGEPGKAGEKGLPGAPGLRGLPGKDGETGAEGPP 575
                                                                                                                                        636 GBRGSPGAQGLQGPRGLPGTPGTDGPKGASGPAGPPGAQGPPGLQGMPGBRGAAGIAGPK 695
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                                                                                                                  GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
                                                                                                                                                                                             414 ------PGPTGLP-----APPGERGGPGSRGFGADGVAGPKGPA 447
                                                                                                                                                                                                                                                                       -----PGPAGPKGSPGEAGRPGEAGLPGAKGLIGSP 483
                                                                                                                                                                                                                                                                                             7.56 GETGPPGTSGIAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 815
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  GPKGAPGERGPSGLAGPKGANGDPGRPGEPGLPGARGLTGRPGDAGPQGKVGPSGAPGED 515
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M9-DOS
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                          685 GSPGSPGPDGKTGPPGP-----AGODGRPGPPGPPGARGOAGVMGFPGPKGAAGEP 735
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Search completed: October 18, 2004, 13:44:02 Job time : 39.5431 secs

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October 18, 2004, 13:42:06; Search time 105.622 Seconds (without alignments) 2513.149 Million cell updates/sec
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GenCore version 5.1.6
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	80	Sequence 8, Appli	Sequence 20, Appl	Sequence 11, Appl	Seguence 8, Appli	Sequence 10, Appl	Sequence 21, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 150, App	Seguence 25, Appl	Sequence 243, App	Sequence 16, Appl	Sequence 261, App
QΙ	US-10-402-089-8	US-10-402-072A-8	US-10-104-889-20	US-10-104-889-11	US-10-104-889-8	US-10-104-889-10	US-10-216-705-21	US-10-357-851-1	US-10-358-024-1	US-10-788-792-150	US-10-468-091-25	US-10-291-265-243	US-10-104-889-16	US-09-918-715-261
DB	15	15	15	15	15	15	14	16	16	17	16	14	15	10
% Query Match Length	1449	1449	1057	1107	1171					1464		1464	1057	1464
% Query Match	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.5	59.5	59.5	59.4
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Sequence 8, Application US/10402089
| Sequence 8, Application US/10402089
| Publication No. US2004000563A1
| GENERAL INFORMATION:
| APPLICANT: Bell, Marcum P. APPLICANT: Bell, Thomas B. APPLICANT: Seeley, Todd W. ITLE OF INVENTION: PORCINE COLLAGENS AND GELATINS FILE REFERENCE: PP0402.3 CON CURRENT APPLICATION NUMBER: US/10/402,089
| CURRENT FILING DATE: 2003-03-26
| PRIOR APPLICATION NUMBER: US 09/709,700
| PRIOR FILING DATE: 2000-11-10
| NUMBER OF SEQ ID NOS: 72
| SOFTWARE: Patentin version 3.2
| SEQ ID NOS BLENGTH: 1449
| TYPE: PRI
| CRGANISM: Sus scrofa
| US-10-402-089-8
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Best Local Similarity 56.7%
Matches 559; Conservative
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US-10-402-072A-8

US-10-402-072A-8

Sequence 3, Application US/10402072A

Publication No. US20040018592A1

GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Neff, Thomas B.
APPLICANT: Refer, Thomas W.
APPLICANT: Polarek, James W.
APPLICANT: Polarek, James W.
APPLICANT: POSELOY, Todd W.
CURENT APLICATION WOWBER: US/10/402,072A

CURRENT APPLICATION NUMBER: US/10/402,072A

PRIOR APPLICATION NUMBER: US 09/709,700
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                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                    Length 1449;
                                                                                                                                                                                                                                            Indels 169;
                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                 59.6%; Score 2765.5; DB 15
56.7%; Pred. No. 4.5e-131;
ive 32; Mismatches 226;
                                                                                                                                                                                                                                                                                         ---RGFPGA---
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PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SOFFWARE: Patentin version 3.2
SEQ ID NO 8
                                                                                                                                                                                               Query Match
Best Local Similarity 56.7
Matches 559; Conservative
                                                                                     LENGTH: 1449
TYPE: PRT
ORGANISM: Sus scrofa
                                                                                                                                                         US-10-402-072A-8
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	218 GLEGPPGERGGPGSRGFPGADGVAGPRGFRGSFPGFAGFRGSFPGEAGLFGAK 377	558 GSQCAPGIQCMPGERGAAGLEGPKGDACKGADGSPGCBCGACAGAP 475 GAKGLTGSPGSPGDCKTGPPGPAGGDCRPGPARGQ 618 GDKGESGPSGPAGTCACRFGPAGDACRFGPPGARGQ 618 GDKGESGPSGPAGTCACRFGPAGAGAGACAGACAGAAGAAGAAGAAGAAGAAGAAGAAGAA	RESULT 4 US-10-104-889-11 Sequence 11, Application US/10104889 Sequence 11, Application No. US20040086961A1 GENERAL INFORMATION: BUEGITER, DOUGLAS BROKAW, JANE TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: DILWORTH & BARRESE STREET: 333 BARLE OVINGTON BOULEVARD CITY: UNIONDALE STATE: NY COUNTRY: U.S.A.
Qy 759 AGAQGPPGP	RESULT 3 US-10-104-889-20 i Sequence 20, Application US/10104889 i Sequence 20, Application US/10104889 i GENERAL INFORMATION: APPLICANT: GRUSKIN, ELLIOT A. BUECHTER, DOUGLAS BROKAW, JANE ZHANG, GVANGHUI PADLELLA, DAVID I TITLE OF INVENTION: AMINO ACID MODIFIED FOLYPEPTIDES NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESSE: ADDRESSER: DILMORTH & BARRESE	CITET. 333 EARLE OVINGTON BOULEVARD CITY: UNNONDALE STATE: NY CONDUTE: NY CONDUTE: NY CONDUTE: LISS3 COMPUTER: Flopy disk COMPUTER: Flopy disk COMPUTER: TEM PC compatible CORPUTER: TEM PC compatible CORPUTER: TEM PC compatible CORPUTER: TEM PC compatible CORPUTER: LEM PC compatible COMPUTER: LEM PC compatible CORPUTER: LEM PC compatible COMPUTER: LEM COMPATION COMPATION COMPUTER: LEM COMPATION COMPATION COMPUTER: LEM COMPATION COMPATION COMPUTER: LEM COM	Query Match 59.6%; Score 2765; DB 15; Length 1057; Best Local Similarity 55.4%; Pred. No. 3.8e-131; Matches 19; Qy 1 GPPGEPGPTGLPGPPGRAGPGRGPGPGRGPGPGPGPGPGPGPGPGPGPGPG

917 771 977

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562 GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
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                                                                                               ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP
                                                                                                                                                                  678 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP
                                                                                                                                                                                                                                                                                              736 GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----
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Publication No. US20040086961A1

GENERAL INFORMATION:
GENERAL INFORMATION:
BUECHTER, DOUGLAS
BROKAW, JAME
ZHANG, GUANGHUI
PAOLELLA, DAVID

IITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDER ADDRESS:
BUEDRESSEE: DILMORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STRATE: NY
STATE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PS attentin Release #1.0, Vers
SOFTWARE: PS attentin Release #1.0, Vers
CURRENT APPLICATION DATA: 2002
CLASSIPICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY ARENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELESPONE: (516) 228-884
TELESPONE: (516) 228-8816
INFORMATION POR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-104-889-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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LENGTH: 1171 amino acids
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGPPGAR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 GPMGPSGPRGLPGPPGAPGPQGFQGPPGEPGASGPMGPRGPPGPPGKNGDDGEAGKP 77
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                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GPSGPA-
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                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-6484
TELEPRAX: (516) 228-6484
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-104-889-11
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TYPE: amino acid
STRANDEDNESS: single
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GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAQPKGSPGEAGRPGEAGLPGAK 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192;
                                                                                       APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
BROKAM, JANE
ERANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SECUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: DILMORTH & BARRESE
STREET: 333 EARLE CVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                 ZIP: 11553

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.6%; Score 2765; DB 15; 55.4%; Pred. No. 4.6e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FLING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWNERS
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNES: single
CTPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-104-889-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: STEEN, JEFFREY S
TELECONTULICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
                                    Sequence 10, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                STATE: NY COUNTRY: U
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Best Local Simil
Matches 561; C
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                                        Gaps
                                                                         GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA--
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                                      Indels
'Match 59.6%; Score 2765; DB 15;
Local Similarity 55.4%; Pred.'No. 4e-131;
les 561; Conservative 31; Mismatches 228;
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 Query Match
Best Local S:
Matches 561
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Tue Oct 19 09:28:00 2004

		AGSPGFQGLPGPA AAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS	Qy 181 GPPGEAGKPGECQVPGDLGAPGPSGPAGEPGPT 213	Qy 214 GLPGPPGERGGPGSRGFPGADGVAGFKGPAGERGSPGPAGFKGSPGEAGRPGEAGLPGAK 273 Db 479 GLPGPFGERGGPGSRGFPGADGVAGFKGPAGFKGSPGPAGFKGSPGPAGFKGSPGEAGLPGAK 538	Qy 274 GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 333	Qy 334 GVPGPPGAVGPAGKDGEAGAQGPPGPAGERGEQGPAGSPGFQGLPGFAGPPGEAGKP 393	Qy 394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPP 423	QY 424 GERGGPGSRGFPGADGVAGPKGBRGSPGPAGPKGSPGEAGRPGEAGLP 474 :	OY 475 GAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ 515	OY 516AGUMGFPGPKGAAGEPGXAGERGVPGPPGAVGPAGKDGEAGAQGPP 561	Oy 562 GPAGPAGERGEQGPAGSPGFOGLPGPAGPPGEAGYPGEQGYPGDLGAPGFSGPAGEP 618	QY 619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEA 675	Qy 676 GLPGAKGLTGSPGSPGRPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEP 735	Oy 736 GKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPA 771	772	Db 1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1190	RESULT 8 10-350-351-01 20-10-357-851-1 2 Sequence 1, Application US/10357851 2 Publication No. US20040151731A1 3 GENERAL INFORMATION:
GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 377 GLTGSPGSPGSPGFPGPGAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 33. [334 438 304	5.94 GEQGVPGDLGAPGESSFAGE 4.98 GEQGVPGDLGAPGPSGARGERGFPGBRGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP 4.98 GEQGVPGDLGAPGPSGARGERGFPGBRGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP 4.94 GEPGCPGCPGAPGAPGGRAGBRGSPGCPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGP	SS8 GSQGAPGLQCMPGERGAAGIPGPRGDAGPRGDAGPRGDGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	DGRPCPPGPRGAKGO 	SAGAQGPP NAGPPGPP	QY 562 GPAGPAGERGEQGPAGSPGFQGLPGPAGPFGEAGKPGEQGVPGDLGAPGPSGPAGEP 618	Qy 619 GPTGLPGPPGERGCPGSRGFPGADGVAGPRGERGSPGPAGPKGSPGEAGRPGEA 675	PGPAGODGRPGPPGPPGARGOAGVMGFPGPKGAAGEP 	Qy 736 GKACERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPA 771	Oy 772 GERGEGGPAGSPGFQGLPGPAGPPGEAGKPGEGGVPGDLGAPGPSGPAG 820	RESULT 7 US-10-216-705-21 ; Sequence 21, Application US/10216705	ш ()	; TITLE OF INVENTION: obtaining Such and Their Uses ; FILE REFERENCE: 1149-3 DIV ; CURRENT APPLICATION UMBER: US/10/216,705 ; CURRENT FILING DATE: 2002-08-09		; SOFIWAKE: Patentin Version 3.1 ; SEQ ID NO 21 ; LENGTH: 1464 . TYDE: DRT) ORGANISM: Homo sapiens US-10-216-705-21	Query Match 59.6%; Score 2765; DB 14; Length 1464; Best Local Similarity 55.4%; Pred. No. 4.8e-131; Matches 561; Conservative 31; Mismatches 228; Indels 192; Gaps 19; Qy 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSFGEA 57

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1079 GPAGARGPAGPOGPRGDKGETGEOGDRGIKGHRGFSGLQGPPGPPGSPGSPGGPSGASGPA 1138
959 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP 1018
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                               676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGARGQAGVMGFPGPKGAAGEP
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                                                                                                                                                                              772 GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1464;
                                                                                                                                                                                                                                                                   Sequence 1, Application US/10358024
Publication No. US20040151732A1
GENERAL INFORMATION:
APPLICANT: Jicha, Douglas L.
APPLICANT: Pelsue, Stephen
TITLE OF INVENTION: T-Lymphocytes Reactivity with Collagen
FILE REPERENCE: 13436US
CURRENT APPLICATION UNMBER: US/10/358,024
CURRENT APPLICATION NOWBER: US/2004
CURRENT PELSONE: 2003-02-04
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
59.6%; Score 2765; DB 16;
Best Local Similarity 55.4%; Pred. No. 4.8e-131;
Matches 561; Conservative 31; Mismatches 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1464
TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-358-024-1
                                                                                                                                                                                                                                          RESULT 9
US-10-358-024-1
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      APPLICANT: Jicha, Douglas L.

TITLE OF INVENTION: Method and Compositions Involving
TITLE OF INVENTION: T-Lymphocyte Reactivity with Collagen in Aortic Tissue
TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients
FILE REPERSENCE: 13376US
CURRENT APPLICATION NUMBER: US/10/357,851
CURRENT FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 3
SOFTRARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Publication No. US20040157329A1
Publication No. US20040157329A1
Publication No. US20040157329A1
Publicature De Department of Sydney
TITLE OF INVENTION: Matrix gene expression in chondrogenesis
FILE REFERENCE: 50031.08-13
CURRENT FILING DATE: 2003-08-13
PRIOR APPLICATION NUMBER: US/10/468,091
PRIOR PILING DATE: 2001-02-15
PRIOR PEDICATION NUMBER: AU PR3116
PRIOR PLOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
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US-10-788-792-150
is dequence 150, Application US/10788792
sequence 150, Application US/10788792
sequence 150, Application US/10788792
sequence 150, Application No. US20040191819A1
septicant: Bayer Pharmaceuticals Corporation
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septicant Septicanton Number: US/10/788,792
current Filing Date: 2004-02-27
septicant Philos Date: 2003-02-28
software: Patentin version 3.2
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GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP
                                                                       719 GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 561; Conserv
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US-10-788-792-150
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                                                                                                                                                                                      US20030232054Alel Nucleic Acids and Polypeptides
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                  Indels 192;
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GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                                                   APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION:
TITLE OF INVENTION: NUMBER: US/10/291,265
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-3
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-15
                                                                                                          ; Sequence 243, Application US/10291265; Publication No. US20030232054A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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LENGTH: 1464
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4atches 560; Conservative
     ; LENGTH: 1461;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-468-091-25
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                                                                                                                                                                                                                  GRPGEAGLP---GAKGLIGSPGSPGP-----DGKIGPPGPAGODGRPGPPGAR
                                                                                                                                                                                                                                                                             106 GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA-----GKDGEAGAQ
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                                                                                     59.5%; Score 2759; DB 15; 55.3%; Pred. No. 7.5e-131; ive 31; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEOGVPGDLGAPGPSGPAGE------PGP-
                                       16
     TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
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Les 560; Conserv
                                                    US-10-104-889-16
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                                                                                                                                                                                                                                           GPIGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP----KGSPGEAGRPGEA 675
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475 GAK-----GLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGARGQ------
                                                                                                               516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP
                                                                                                                                             839 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP
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OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
R OF SEQUENCES: 50
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                                                                                                                                                                                                                                                                                                                                                                           -----AGAQGPPGP-
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STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER: US/09/169,768
LING DATE: 09-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          GKAGERGVPGPPGAVGPAGKDGE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/10104889
Publication No. US20040086861A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BROKAW, JAME
BROKAW, JAME
ZHANG, GUANGHUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 16:
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
TENCTH: 1057 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 11553
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-104-889-16
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                                                                             179 GPWGPSGPRGLPGPPGAPGPQGFQGPPGBPGRPGASGPWGPRGPPGPPGRAGDDGBAGKP
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                                                                                                                                            516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP
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719 GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Branch. Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lauso, Michael J.
APPLICANT: Lodges, Michael J.
APPLICANT: Lodges, Michael J.
APPLICANT: Dereing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jang, Yudiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REPRENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEC ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 159
LENGTH: 1464
TYPE: PRT
CREANTSM: Homo sapiens
US-10-060-036-159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 159, Application US/10060036; Publication No. US20030073144A1; GENERAL INFORMATION:
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       GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
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Best Local Similarity 55.2%; Pred. No. 1.5e-130;
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Search completed: October 18, 2004, 13:58:35 Job time: 112.622 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 18, 2004, 13:31:10 ; Search time 32.5431 Seconds (without alignments) 2427.363 Million cell updates/sec Run on:

US-10-658-989A-3 4640 I GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 821 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	RESULT 1 CGHUIS collagen alpha 1(I) chain precursor - human N,Alternate names: procollagen alpha 1(I) chain
	C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004 C;Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S1 S269; A29439; I53466; A02852; I37247 R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
	Gene 67, 105-115, 1988 A,Title: Complete nucleotide sequence of the region encompassing the first twenty-five A,Reference number: I60114; MUID:88329734; PMID:2843432
	Afactesion: translated from GB/EMBL/DDBJ A;Status: translated from GB/EMBL/DDBJ A;Residues: 1-369,'L','371-589 < DAL> A;Residues: 1-369,'L','371-589 < DAL> A;Cross-references: UNIPROT:PO2452, UNIPROT:Q14992; UNIPROT:Q16053; UNIPROT:Q13896; UNI
	R;Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Proc Biochem. J. 253, 919-922, 1988 A;Title: Structure of a full-length cDNA clone for the prepro-alpha-1(1) chain of human A;Reference number: S01143; MUID:89025644; PMID:3178743
	A;Accession: S01143 A;Molecule type: mRNA A;Residues: 1-472 <tro 1-472="" <tro="" a;aresidues:="" a;aresidues:<="" td=""></tro>
	ANCHES TELETELECT IN THE EMBL/Gener, NIT. 337012; FIDNICASO VIII.; FIDISTOLE; GENERALIS, NIT. 8, NOTE: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-UUN-1988 R;Chu, M.L., de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C Nature 310, 337-340, 1984
•	A;Title: Human proalpha!(I) collagen gene structure reveals evolutionary conservation o A;Reference number: A93335; MUID:84270697; PMID:6462220 A;Accession: A93335 A;Accession: A93335 A;MOID:842706:10 A;MOID:84
	A; Residues: 1-58, 'Q', 60-181 < CHU> A; Residues: 1-58, 'Q', 60-181 < CHU> A; Cross-references: EMBL: X00820; NID: 935657; PIDN: CAA25394.1; PID: 935658 B; Rossouw, C.M.S.; Vergeer, W.P.; du Plocy, S.J.; Bernard, M.P.; Ramirez, P.; de Wet, W
	J. BIOL. Under Zoz, ISLETISES, 1997, A;Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene en A;Feference number: ISS2S4; MUID:88033098; PMID:2822714
	A; Status: translation not shown; translated from GB/EMBL/DDBJ A; Molecule type: DNA
	A;Kesiques: 1-45 <kous> A;Cross-references: GB:J02829; NID:g180387; PIDN:AAAS1993.1; PID:g180388 R;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.</kous>
	A,Title: Regulatory elements in the first intron contribute to transcriptional control A,Reference number: A39943; MUID:88097389; PMID:3480516 A,Reference number: A39943; MUID:88097389; PMID:3480516 A,Accession: A39943 A,MOID:874006 NMA
	A;Residues: 1-34 <bor> A;Residues: 1-34 <bor> A;Cross-references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238 R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.</bor></bor>

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A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mSN01229, MID:9180391; PIDN:4AA51995.1; PID:9180392 A; Molecule sequence partially completed for missing nucleotides by A29439 A; Molecule sequence partially completed for missing nucleotides by A29439 A; Molecule to Molec
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A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Rolecules: 472-594, R., 596-607 < CH3>
A,Cross-references: GB:K03178; GB:K03179; NID:g179612; NID:g179613; PIDN:AAA51847.1; PID
A,Note: the authors translated the codon CGT for residue 595 as Pro
R,Mallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A,Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 710-720, fB',722-737, 'E',739-745 «WAL>
A;Molecule type: mRNA
A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A;Note: Lolezti, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes
Hum. Mol. Genet. 3, 2201-2206, 1994
A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the CA;Reference number: I54365; MUID:95187161; PMID:7881420
                    A/Accession: I52905
A/Status: translated from GB/EMBL/DDBJ
A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Residues: 342-352, 'C',354-359 <WI2>
A/Cross-references: GB:S64717; NID:g408195; PIDN:AAB27677.1; PID:g408196
A/Cross-references: GB:S64717; NID:g408195; PIDN:AAB27677.1; PID:g408196
B/A/Cross-reference from patient with osteogenesis imperfects
B/A/Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
B/A/Eltle: Nucleoride sequences of complementary deoxyribonucleic acids for the proalphal
A/Reference number; A90476; MUID:84080385; PMID:6689127
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A; Residues: 1179-1387, R', 1389-1464 <CH7>
A; Experimental source: fetal cell 88-251
R; Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Ni
D. Biol. Chem. 253, 14650-14607, 198
A; Title: Substitution of Cysteine for Glychne within the Carboxyl-terminal Telopeptide
A; Reference number: 155269; MUID:89008319; PMID:3170557
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A;Molecule type: DNA
A;Redues: '46-766', '87, 76-781 <-787 |
A;Residues: '46-766', '87, 76-781 <-787 |
A;Cross-references: GB:L47667; NID:g1009093; PIDN:AAB59576.1; PID:g1009094
B;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J Boll Chem. 268, 18218-18225, 1993
A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of a A;Reference number: A47426; MUID:93352646; PMID:9349697
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;Residues: 1179-1276, 'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
;Cross-references: GB:S64596; NID:G407589; PIDN:AAB27856.1; PID:G407590
;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
;Note: does not represent an experimentally determined sequence but three different
;Accession: B47426
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Residues: 1179-1276,'H',1278-1464 <CH5>
Experimental source: fetal cell 86-237
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Residues: 1179-1336,1339-1464
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A;Molecule type: DNA
A;Residues: 1-34 <CH2>
A;Residues: 1-34 <CH2>
A;CH2S-S: 1-34 <CH2S-S: 1-3
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A,Reference number: A35233; MUID:90202908; PMID:2318855
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A; Title: A base substitution in the exon of a collagen gene causes alternative splicing A; Reference number: 809400; MUID: 89356643; PMID: 2767050
J. Biol. Chem. 260, 2315-2320, 1985
Affitle: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter
A;Reference number: I55237; MUID:85130970; PMID:2857713
A;Accession: I55237
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                                                                                                                                                                                                                                              -GKDGEAGAQ
                                                                                                                                                                                                                                                                                                                                    ------AGSPGFOGLPGPA
                   A, Molecule type: DNA
A, Residues: 1187-1194, C', 1196-1220 <COH>
A, Rosaldues: 1187-1194, C', 1196-1220 <COH>
A; Cross-references: GB:W23213; NID:G340842; PIDN:AAB59363.1; PID:G499622
A; Note: mutant sequence from a patient with mild osteogenesis imperfecta
A; Note: mutant sequence from a patient with mild osteogenesis imperfecta
A; Nacelae, T., Rasassina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A; Title: Human pro-alpha-1(1) collagen: cDNA sequence for the C-propeption
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                                                                                                                     Query Match

59.4%; Score 2756; DB 1;
Best Local Similarity 55.3%; Pred. No. 3.5e-130;
Matches 560; Conservative 31; Mismatches 229;
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A;Status: translated
A;Molecule type: nwn
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A, Accession: A2392

A, Moclestule type: mRNA

A, Residues: 1518-1128 e RENA

A, Cross references: GB:NI4423; NID:G192261; PIDN:AAA37333.1; PID:G192262

R; Monson, U.M.; Friedman, J.; McCarthy, B.J.

M, Cell. Biol. 2, 1362-1371, 1982

A, Accession: 149559

A, Cross references: GB:NI1491; NID:G192263; PIDN:AAA37334.1; PID:G192264

R; Marber, K.; Kuehn, M.; Delius, H.; Janensch, DBJ

A, Accession: 149557

A, Accession: 149557, MUD:G192263; PIDN:AAA37334.1; PID:G192264

R; Marber, K.; Kuehn, M.; Delius, H.; Janensch, B.J.

A, Accession: 149557, MUD:G192246; PIDN:AAA37330.1; PID:G192264

A, Accession: 149557

A, Accession: 149557

A, Accession: 149557, MUD:G192246; PIDN:AAA37330.1; PID:G553881

A, Accession: 149557

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A, Accession: 149587

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A;French, B.T.; Lee, W.H.; Maul, G.G.
Gene 39, 311-312, 1988
A;Title: Nucleotide sequence of a cDNA clone for mouse proalphal(I) collagen protein.
A;Reference number: A23982; MUID:86137403; PMID:3841523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
S21626
collagen alpha 1(I) chain precursor - mouse
collagen alpha 1(I) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R;Li, S.W.; Kthilan, J.; Prockop, D.J.
A;Title: The complete CDNA coding sequence for the mouse pro-alpha-1(I) chain of tyn
A;Reference number: S57243
A;Accession: S57243
A;Accession: S57243
A;Accession: S7243
A;Accession: Diphys. Acta 1089; 241-243, 1991
B;Accinic B;Dobys. Acta 1089; 241-243, 1991
A;Title: Specific hybridization probes for mouse type I, II, III and IX collagen mRi
A;Reference number: S16374
A;Accession: S5724
A;Accession: S7724
A;Accession: S7724

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                                                                 171
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                                                                                                                                                                                                                      GERGEQGPAGSP---GPQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                       GKAGERGVPGPPGAVGPAGKDGE
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A;Residues: 1442-1453 <MET>
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                                                                                                                                                                                                                                                                                                                                                        1139
                 736
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A;Cross-references: EMBL:X54876; NID:g50486; PIDN:CAA38657.1; PID:g50487 C;Genetics: A;Gene: COL1A1	
A; Introns: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/ C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; K; Keywords: coiled coil; extractellular matrix; glycoprotetin; heterotrimer; triple helix F; 1-22/Domain: signal semience #feration predicted corp.	Qy 747
F;23-151/Domain: amino-terminal propertide flatus predicted <pro> F;30-89/Domain: von Willebrand factor type C repart homology <vwc> F;152-1453/Product: collagen alpha 1(I) chain #status predicted <mat> F;1224-1453/Domain: fibriliar collagen carboxyl-terminal homology <fcc></fcc></mat></vwc></pro>	QY 784GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
Gaps 16;	RESULT 3 CCCH1S collagen alpha 1(1) chain - chicken (tentative sequence) (fragments)
OY 1 GPPGEPGPTGLPCPPGERGGPGSRGFPGADGVAGPKGPAGFRGSPGPA 48	C;Species: Gallus gallus (chicken) C;Date: 12-Aug-1981 #sequence revision 06-Jul-1982 #text_change 31-Mar-2000 C;Accession: A90458, A90181, A02857 R;Highberger, J.H.; Corbett, C; Dixit, S.N.; Yu, W.; Sever, J.M.; Xang, A.H.; Gross, J.
QY 49 GPKGSPGBAGRPGBAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 93	ite pri
QY 94 GRPGPPGPARGQAGVMGFPGFKGAAGEPGKAGERGVPGPPGAVGPAGKDGEA 147 DD 300 GRPGPPGTAGARGNDGAVGAAGPPGPTGPTGPTGPTGPTGAVGAKGEAGPQGARGSEGPQGVR 359	A;Molecule type: protein A;Residues: 1-1036 <hig> A;Experimental source: skin A;Note: this is the latest in a series of papers from these workers elucidating the secu</hig>
QY 148 GAOGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ 192 Db 360 GEPGPPGPAGAAGPAGAPGANGANGAPGIAGAPGFPGARGPSGPQGFSGPPGPK 419	the
QY 193 GVPGDLGAPGPSGPAGEPGFTGLPGFPGERGGP 225 Db 420 GNSGEPGAPGNKGDTGAKGEPGATGVQGPPGPAGEEGKRGARGEPGPPGERGGP 479	A;Accession: A90181 A;Molecule type: protein A;Residues: 1037-1042 <eyr> A;Experimental source: skin</eyr>
Oy 226 GSRGFPGADGVAGPKGPAGERGSPGAGKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD 285	A;Note: residues 1037-1042 above correspond to the carboxyl end of the protein C;Comment: Lysines at positions 103, 700, 934, and 946 above may be hydroxylated in some C;Comment: Most of the prolines at the third position of the tripeptide repeating unit (C;Comment: Pro-1002 is the only 3-hydroxyrolline and the only hydroxylated proline in po
Oy 286 GKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA 345	omolog trimer
	Query Match 57.7%; Score 2679; DB 1; Length 1042; Best Local Similarity 53.7%; Pred. No. 1.8e-126; Matches 540; Conservative 30; Mismatches 250; Indels 186; Gaps 16;
	OY 1 GPPGEPGPTGLPGPPGERGPGSRGFPGADGVAGPKGPAGBR 42
	QY 43 GSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD93
	OY 94GRPGPPGARGQAGVMGFPGPKGAAGBPGKAGERGVPGPPGAVGPA 141
	OY 142 GKDGEAGAQSPRGPAGBRGEQGPAGSPGFOGLPGPAGPPGEA 186
	Oy 187 GKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPP 219
00	Qy 220 GERGGPGSRGFPGADGVAGFKGPAGERGSPCAPAGFKGSPGEAGRPGBAGLPGAKGLTGSP 279
	OY 280 GSPQPDGKTGPPGPPGPPGPPGPPGARGOACVMGFPGPKGAAGEPGKAGERGVPGPP 339

333 GSPGPDGATGPPGPAAGQCRPGAAGACACACACACACACACACACACACACACACACACA
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Reference

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Eur. J. Blochem. 234, 125-131, 1995

A; Tille: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil car A; Accession: 863514; MUID: 96096730; PMID: 8529631

A; Accession: 863514

A; Molecule type: protein

A; Molecule type: protein

A; Residues: 233-261;575-590;756-763, XX, 765-779 <FRA>

R; Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, A; Litler, G.E.; Mas-splicing mutation (G+SIVS20) in the type II collagen gene (COL2A1) in a A; Reference number: 138867; MUID: 95150028; PMID: 7847372
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A; Residues: 630-640, 'A', 642-785 «VIKZ»
A; CROSS-TEFERORGES: EMBL:X16158 | NID:92951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA3427
PIDN:CAA34283.1; PID:91335023; PIDN:CAA34284.1; PID:91335024
R; Bogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D
A; Title: An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain pro
A; Reference number: A44309; MUID:93054548; PMID:1429602
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Proc. Natl. Acad. Sci. U.S.A. 87, 3889-3893, 1990

NTILLE Tandem duplication within a type II collagen gene (COL2AI) exon in an individua NRESERENCE number: S16502; MUID:90251662; PMID:2339128
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A; Residues: 1164-1184, GPSGKDGANGIPGPI',1185-1199 <TILZ>
A; Cross-references: EMBL:M37126; NID:g180808; PIDN:AAAS2037.1; PID:g180809
A; Notes: mutant sequence from a patient with spondyloepiphyseal dysplasia
R; Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
A; Cheah, K.S.E.; Gai. U.S.A. 82, 2555-2559, 1985
A; Title: Identification and characterization of the human type II collagen gene (COL2A1)
A; Reference number: A02858; MUID:85190534; PMID:3857598
                                    P.; Herbage,
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A; Residues: 1175-1487 <ELI>
A; Cross-references: EMBL:X06268; NID:g30096; PIDN:CAA29604.1; PID:g30097
A; Experimental source: Letal epiphyseal cartilage
R; van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
Biochem. J. 237, 922-925, 1986
A; Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.
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              S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, siochem. 234, 125-131, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 40,'G',42-456,'E',458-480,'P',482-509 <TILL>
A;Cross-references: EMBL:U15195; NID:9557053; PIDN:AAB60370.1; PID:9557054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Moseidues: 501-676, 'A', 678-783, 'A', 785-831, 'PA', 834,'F', 836-1214 < RAM>
A; Cross-references: EMBL:X13783; NID:g30037; PIDN:CAA32030.1; PID:g930050
R; Vikkula, M.; Pelconen, L.
FEBS Lett. 250, 171-174, 1989
A; Title: Structural analyses of the polymorphic area in type II collagen g
A; Reference number: S05000; WUID:89325561; PMID:2753125
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A; Residues: 1032-1056, Nv, 1058-1068, TT', 1070-1487 < CHE>
A; Cross-references: GB: J00116; NID: g180395; PIDN: AAA51997.1;
R; Ellima, K; Vuorio, T; Vuorio, E.
Nucleic Acids Res. 15, 9499-9504, 1887
A; Fitle: Determination of the single polyadenylation site of
A; Reference number: A27280; MUID: 88067771; PMID: 2825137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 440,'G',4
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A; Residues: 1-28 < VIX.>
A; Residues: 1-28 < VIX.>
A; Cross-references: EMBL:XS8709; 'GB.S40537; NID.g35659
A; Note: this translation is not annotated in GenBank entry HSPROCOE1, release 111.0
B; Nunez, A.M.; Kohno, K.; Martin, G.R.; Yamada, Y.
Gene 44, 11-16, 1986
A; Title: Promoter region of the human pro-alpha-1-(II)-collagen gene.
A; Reference number: A24828; MUID:87031574; PMID:3021582
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A;Molecule type: protein
A;Residues: 188-189,'X',191-195;1224-1230,'X',1232-1236 <DIA>
number: A38513; MUID:91184811; PMID:2081599
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                                                                                                                                 lecule type: DNA
sidues: 1-103 <RYA>
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A41182

collagen alpha 1(II) chain precursor - mouse

collagen alpha 1(II) chain precursor - mouse

collagen alpha 1(II) chain precursor - mouse

cyspecies: May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999

Cybate: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999

Cyaccession: A41182, A44885

RyMetsacranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.

A; Metsacranta, M.; Toman, D.; de Cromprugghe, B.; Vuorio, E.

A; Mitle: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A; Reference number: A41182

A; Acteus: preliminary; not compared with conceptual translation A, Molecule type: DNA A, Residues: 1.1419 < MET> A, CCOS = references: GB: M65161 R, CCOS = references: GB: M65161 R, CCOS = response to the mouse alpha 1(II) collagen gene is not restricted to cartila. A, Reference number: A44885; MUID: 91347939; PMID: 1879363 A,Molecule type: DNA A,Residues: 1-28 «CHE» A,FCross-references: GB:563190, NID:9234368, PIDN:AAB19627.1; PID:9234369 A,Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192) C,Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology

23 B GPKGPAGERGSPGPAGPKGSPGEAGRPGBAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 297

465 GEGGERGEPGPAGPGGAPGPAGEEGKRGARGEPGGVGPIGPPGERGAPGNRGFPGQDGLA

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Specials: Mas Macoulus Michael Mouse; Specials: Mas Macoulus Michael Mouse; Ja-May-1992 #text_change 09-Jul-2004
C; Accession: B41182
Reference and May 1991
A; Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A; Reference number: A41182; MUD:91384489; PMID:1885613
A; Reference number: A41182; MUD:91384489; PMID:1885613
A; Reference number: A41182; MUD:91384489; PMID:1885613
A; Reference number: A41182; MUD:913584489; PMID:1885613
A; Reference number: A41182; MUD:91358489; PMID:1885613
A; Reference number: A41182; MUD:91358489; PMID:1885613
A; Reference number: A41182; MUD:9133; GB:M65161
C; Superfamily: collagen a1[1] chain; fibrillar collagen carboxyl-terminal homology; RYGC>
F; A33-91/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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50.6%; Pred. No. 1.7e-115;
iive 49; Mismatches 271; Indels 168; Gaps
                                                                                                                     collagen alpha 1(II) chain precursor (long splice form) - mouse C;Species: Mus musculus (house mouse)
1117 GPPGPRGRSGETGPVGPPGSPGPPG 1144
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Best Local Similarity 50.64
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C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
F;1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                        GNPGEPGEPGVSGPMGPRGPPGPAGKPGDDGEAGKPGKSGERGLPGPQGARGFPGTPGLP 216
                                                                                                                                                                                                                                                                                                                        217 GVKGHRGYPGLDGAKGEAGAPGVKGESGSPGENGSPGPMGPRGLPGERGRTGPAGAAGAR 276
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                                                                     53.0%; Score 2460; DB 2; I
50.6%; Pred. No. 1.6e-115;
iive 49; Mismatches 271;
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ВР	885 GARGAQGPPGATGFPGAAGRVGPPGANGNPGPAGFPGPAGKDGPKGVRGDSGFPGRAGDP 944	Q	
oy B	583 GIPGPAGPPGERGKPGEGGVPGDIGAPGPSGPAGEPGPTGIPGPPGERGGPGSRGFPGAD 642	상 원	340 GAVGPAGKDGEAGAQGPPGBAGERGEQGPAGSPGFQGLPGPAGPPGEAKFGEQGVP 399
. v. 1		දු දු	400 GDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 456
6 &	GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP 73	े हें	
oy Oy	1065 GAPGAPGPPGSPGPAGPTGKQGDRGEAUAQGPMGPSGPAGAKGIAGFYGGRKGDNGESGEQ 1144 736 GKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGBRGERGEQGPAGSPGFOGLPGPA 792 	R &	GWGFPQFXGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP
qa ,	ĠERGLKĠHŔĠFTĠLQĠLPĠPPĠPSĠDQĠĀSĠPĀĠP	a 8	809 GPSGPPGIVGARGAPGDRGENGPPGPAGFPGADGGSGEKGDQGESGQKGDAGAFGFU 808 562 GPAGPAGERGEOGPAGSPGFPGDIPGPAGPPGBAGKP 597
\$ 8	793 GPPGEAGKPGEGGVPGULGAGPGPGGPAG 820 	ß 6	
RESULT 8		5 G	598 GEGGVPGDLGAP 623
collagen C;Specie C;Date:	n alpha 1(II) chain precursor - African clawed frog ss: Xenopus laevis (African clawed frog) 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	ઠે ઇ	624PGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGARPGE- 674 000 GAPGADGT.PDPSGFPGAPGKGPGSSGTRGPPGVGPPGLTGPSGEPGREGNPGSD 1045
C, Access R, Su, M. J. Cell A, Title:	sion: B40333 W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F. Biol. 115, 565-575, 1991 Expression of two nonallelic type II procollagen genes during Xenopus laevis em	g & i	
A; Refere A; Access	ance number: A40333; MUID:92011898; PMID:1918153 iion: B40333	8 8	
A; Molecu A; Residu	116 type: mRNA / / / / / / / / / / / / / / / / / / /	- අධ	
A;Cross-C;Superf C;Keywor F;37-96/ F;1258-1	A;Cross-references: UNIPROT:Q91718; UNIPROT:Q91717; GB:M63595 C;Superfamily: collagen alpha 1(1) chaln; fibrillar collagen carboxyl-terminal homology; C;Reywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix F;37-96/Domain: von Willebrand factor type C repeat homology «VWC» F;1258-1486/Domain: fibrillar collagen carboxyl-terminal homology «FCC»	6 6 6	772 GERGEOGEPAGSPGFOGLPGPPGEAGKPGEOGVPGDLGAPGPSGPAG 820
Query Ma Best Loc	tch 51.7%; Score 2401; DB 1; Length 1486; al Similarity 48.9%; Pred. No. 1.4e-112;	RESULT A40333	9 en alpha 17(II) chain precursor - African clawed frog
Matche Qy	493; CONSETVACIVE 48; MIBMATCHEB 2/0; INUELB 192; Gaps 1 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGER 42	C; Spec	es: Xenopus laevis (African clawed frog) 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
g d		C, Acce R, Su, 1	
જે હ	43 GSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGP 80	A;Refe	A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis e A;Reference number: A40333; MUID:92011898; PMID:1918153 A;Accession: A40333
3 8	1	A;Stat A;Mole	is: nucleic acid sequence not shown unle type: mRNA hine: 1-1492 <nia></nia>
DÞ	329 GLPGERGRPGSSGAAGARGNDGLPGPAGPPGPVGPAGAPGFPGAPGSKGEAGPTGARGPE 388	A; Cros	areferences: UNIPROT:091718; UNIPROT:091717; GB:M63596 areference is presented as substitutions relative to another sequence in a f
ଧୃତ୍ପ ସ୍ଥ	118 GAAGEPGKAGERGVPGPPGANGPAGKDGEAGAGPPGPRGERGEGGPAGSPGFQGLP 177	es the C;Supe C;Keyw	es they replace; the appropriate interpretation of the sequence ingure was reconstructe C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology C; Keywordsa: coilaged coil; extracellular matrix; glycoprotein; trimer; triple helix c: 3.3.6, homein, non willehrand factor type C repeat homology <vwc></vwc>
δλ	178 GPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPP 219	F;3/-5	1492/bomain: fibrillar collagen carboxyl-terminal homology <fcc></fcc>
qa	GPLGPKGETGPPGVAGFKGEQGPKGETGSAGPQGAPGPAGEEGKRGARGEPGAAGPNGPP 5	Query M Best Lo	Query Match 51.5%; Score 2389; DB 2; Length 1492; Best Local Similarity 50.6%; Pred. No. 5.79-112; March Conf. Compositive 50. Mismatches 275; Indels 132; Gaps 14;
රු දු	220 GERGGEGREFANDGVAGPRGPAGERGSPGPAGERGSPGEAGERGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Oy Marc	1 GPPGEPGTTGLPCPPGERGCPGRGFPPADGVAGPXGPAGERGSPC
ò	280 GSPGPDGXTGPPGPAGQDGRPGPPGPPGARCQAGYMGFPGPXGAAGEPGKAGERGVPGPP 339	qq	272 GPPGPQGARGFPGTPGLPGVKGHRGYPGLDGGKGEAGAAGAKGESGASGEAGAPGPRGPR 331

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A,Cross-references: UNIPROT:P04258
R;Dewes, H.; Fietzek, P.P.; Kuchn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A,Title: The covalent structure of calf skin type III c
A,Reference number: A38001; MUID:80026027; PMID:488907
                                                                                                                                                                                                                                                                                      A; Accession: A38001
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Collagen alpha 1(III) chain - bovine
Collagen services: Bos primigenius taurus (cattle)
Colpate: 04-bec-1986 #sequence revision 04-bec-1986 #text change 09-Jul-2004
Colpate: 04-bec-1986 #sequence revision 04-bec-1986 #text change 09-Jul-2004
Colpate: 04-bec-1986 #sequence revision 04-bec-1986 #text change 09-Jul-2004
Ricession: A02862; A38003; A38003; A38004;                                                         | ||:|| | |::| | | ||:|| | ||:|| | ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| |
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A. Accession: A38005; MULD: 80025031; PMLD: 488911.
A. Accession: A38005
A. Molecule type: protein
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A; Molecule type: protein
A; Residues: 423-571 «BEN»
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A; Title: The covalent structure of calf skin type III collagen. A; Reference number: A38003; MUID:80026029; PMID:488909
A; Accession: A38003
A; Molecule type: protein
A; Residues: 572-8803
A; Molecule type: protein
A; Residues: 572-880 «LAN»
B; Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A; Title: The covalent structure of calf skin type III collagen. V. S.
A; Reference number: A38004; MUID:80026030; PMID:488910
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A,Residues: 809-947 <DEW2>
R,Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
HOppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
A,Title: The covalent structure of calf skin type III collagen.
A;Reference number: A38005; MUID:80026031; PMID:488911
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A,Molecule type: protein
A,Residues: 243-422 <DEM1>.
R,Bentz, H.; Fletzek, P.P.; Kuehn, K.
HOppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A;Title: The covalent structure of calf skin type III c
A;Reference number: A38002; MUID:80026028; PMID:488908
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48; Mismatches
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131 GARGANOMERGERGRAPE CATE PAGASARGHORAGES DESCRIPTION OF A CANDER - GROUP - GRO	A; Molecule type: DNA A; Residues: 1-1464 < TONA	A) Closs-Ielelences: UNIFROI:FUGIZI	Submirted to the EMBL Data Library, A;Reference number: \$62120 A;Accession: \$62120	A; Molecule type: DNA A; Residues: 1-866, 'G', 868-1464 <toa;< th=""><th>A; Cross-references: EMBL:X52046; NII R:Metsaeranta, M.: Toman, D.: de Cro</th><th>Biochim. Biophys. Acta 1089, 241-24.</th><th>A; Reference number: S16176; MUID:91.</th><th>A;Status: preliminary A;Molecule type: DNA</th><th>A, Residues: 1442-1464 <met> A, Cross-references: EMBL:X57983; NII</met></th><th>C;Genetics:</th><th>5/3; 673/3; 706/3; 742/3; 760/3; 7 C; Superfamily: collagen alpha 1(1)</th><th>E;1-24/Domain: signal sequence #state</th><th>F:25-124/Domain: propeptide #status F:32-92/Domain: von Willebrand facto F:155-1464/Product: collagen alpha</th><th>F;1236-1464/Domain: fibrillar collac</th><th>Query Match Best Local Similarity 51.4%; Pr</th><th>Matches 477</th><th></th><th>233</th><th>43 GSFGFAGFFGSFGFAGFFGFAGFFGFAGFFGFAGFFGFAGFFGFAGFFGFAGFFGFAGFAG</th><th>66.</th><th>320</th><th>148</th><th>Db 410 GARGPPGPAGTNGIPGTRGPSG</th><th>Qy 208 GEPGFIGLPGPPGERGGPGSRG</th><th>470</th><th>268</th><th>530</th><th>328</th><th>0 0 0</th><th>388</th><th>DD 650 GENGKPGEPGPKGEVGAP</th><th>Qy 448 GERGSPGPAGPKGSPGEAGRPG </th><th>. Oy 508 GPPGARGQAGVMGFPGPKGAAG</th></toa;<>	A; Cross-references: EMBL:X52046; NII R:Metsaeranta, M.: Toman, D.: de Cro	Biochim. Biophys. Acta 1089, 241-24.	A; Reference number: S16176; MUID:91.	A;Status: preliminary A;Molecule type: DNA	A, Residues: 1442-1464 <met> A, Cross-references: EMBL:X57983; NII</met>	C;Genetics:	5/3; 673/3; 706/3; 742/3; 760/3; 7 C; Superfamily: collagen alpha 1(1)	E;1-24/Domain: signal sequence #state	F:25-124/Domain: propeptide #status F:32-92/Domain: von Willebrand facto F:155-1464/Product: collagen alpha	F;1236-1464/Domain: fibrillar collac	Query Match Best Local Similarity 51.4%; Pr	Matches 477		233	43 GSFGFAGFFGSFGFAGFFGFAGFFGFAGFFGFAGFFGFAGFFGFAGFFGFAGFFGFAGFAG	66.	320	148	Db 410 GARGPPGPAGTNGIPGTRGPSG	Qy 208 GEPGFIGLPGPPGERGGPGSRG	470	268	530	328	0 0 0	388	DD 650 GENGKPGEPGPKGEVGAP	Qy 448 GERGSPGPAGPKGSPGEAGRPG	. Oy 508 GPPGARGQAGVMGFPGPKGAAG
	138 GAPGPMGPRGAPGERGRPGLPGAAGARGNDGARGSDGQPGPPGFAGFPGSPGAK 103 GARGQAGWMGFPGPKGAAGEPGKAGERGVPGPPGKDGEA	195 GEVGPAGSPGASSGAPGQRGEPGPQGAAGAPGPPGSDGSPGGKGEMGPAGIPGAPGLI	148 GAQGPPGPAGBAGERGEQGPAGSPGFQGLPGPAGPPGEAGWPGEQGWPGDIGAPGPSGPA	255 GARGPPGFRGVPGQRGAAGEPGKNGAKGDPGPRGERGEAGSPGIAGPKGEDGKDGSP	208 GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGRGFPGEA	315 GEPGANGLPGAAGERGVPGFRGPAGANGLPGERGPPGDRGGPGPAGPRGVAGEPGRNGLP	268 GLPGAKGLTGSPGSPQPDGKTGPPGPAGQDGRPGPPGARGQAGVMGPPGPKGAAGEP	375 GGPGLRGIPGSPGGPGSNGKPGPPGSQGETGRPGPPGSPGPRGQPGVMGFPGPKGNDGAP	328 GKAGERGVPGPPGAVGPAGKDGBAGAQGPPGPAGPAGBAGERGEQGPAGSPGFQGLPGPAGPP	435 GKNGERGGPGGPAGKNGETGPQGPPGPTGPSGDKGDTGPPGPQGLQGLPGTSGPP	388 GEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGGRGFPGADGVA	4.5. GENGING GENGENGENGENGENGENGENGENGERGERGERGERGERGERGERGERGERGERGERGENGENGENGENGENGENGENGENGENGENGENGENGENG		496 GPAGODGRPGPPGPPGARGOAGVNGFPGPKGAAGRPGKAAGERGVP	615 GPAGQPGDKGESGAPGVPGIAGPRGGPGERGEQGPPGPPGPAGFPGAPGQNGEPGARGERGAP	541GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQ	675 GEKGEGGEPGAAGPAGSGPAGPPGPQGVKGERGSPGCPGAAGFPGGRGFPGPGPBANDP	S74 GPAGSPGGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGL-	735 GPPGSSGAPGKDGPPGPPGSNGAPGSPGISGPKGDSGPPGERGAPGPQGPPGAPGIA	624	795 GLTGARGLAGPPGAPGAPGSPGPQGIKGENGKPGPSGQNGERGPPGPQGLPGLAGTAGEP	667 GEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPP	855 GKDGNPGSDGLPGKUGAPGARGDRGENGSPGAPGAPGHPGPPGPVGPRGKDGNGTGPA 712 GDDGNDGCARGNAGDDBKGNAGDDRYNAGDDRYY	915 GPSGAPGPPGSRGPPCPDGRGETGERGAMGIKGHRGFPGNPGAPGSPGNPGAPGPTV	763 GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGBAGKPGBQGVPGDLGAPGPSGPA	975 GSPGPACPRGPVGPSGPPGXDGASGHPGPIGPPGPRGNRGERGSEGSPGHPGQPGPPPGPP	820 G	1035 G 103			mouse	19-Apr-1996 #text_change 09-Jul	-encoding gene: genomic cloning and 09; PMID:7926795

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3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 2
778/3; 796/3; 814/3; 850/3; 868/3; 886/3; 940/3; 976/
chain; fibrillar collagen carboxyl-terminal homology
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Pred. No. 2.1e-111;
Mismatches 266; Indels 129; Gaps
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                                                                                                                     November 1994
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EMBL: X52046
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A Molecule type: mRNA

A. Kosidudes: 149-163, G', 164-240, D', 242-471, D', 473-487, L', 489, S', 491-613, Y', 615-634,

A. Cross-rences: EMBL:X15332; NID:g29545; PIDN:CAA33367.1; PID:g930045

A. Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide

R. Seyer, J.M.; Kang, A.H.

Bochemistry 16, 1154-1144, 1977

A. Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide

A. Reference number: A90399; MUID:77134724; PRID:557335
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A;Residues: 861-1015 <CCL>
A;Cross-references: GB:U65617; GB:M55603; GB:M59227; NID:9180878; PIDN:AAB59383.1; PID:e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: liver
A;Note: author submitted corrections to A90399
R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet. 53, 62-70, 1993
A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
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Blochamistry 11, 3404-3411, 1978
A;Title: Covalent structure of collagen; amino acid sequence of five consecutive CNBr A; Reference number: A90414; MUID:79000343; PMID:687591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      donor site causes skipping of
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A.Filtle: A base substitution at a splice site in the COL3Al gene causes exon A.Reference number: A38303; MUID:91009133; PMID:2145268
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.Residues: 302-423 <CHI>
.Cross-references: GB:S79877; NID:g1195576; PIDN:AAB35615.1; PID:g1195577
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A; Molecule type: DNA
A; Realduse: 357-605 - 6.1E5>
A; Costudes: 357-605 - 6.1E5>
A; Costudes: 357-605 - 6.1E5>
A; Costudes: 357-605 - 6.1E5>
A; Cross-references: GB:M59312; NID:9180815; PIDN:AAA52041.1; PID:9180816
R; Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A; Title: Covalent structure of collagen: amino acid sequence of alphal (IAR Exerence number: A90438; MUID:80198282; PMID:6246925
A; Accession: A90438
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/Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
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A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEY1>
A;Experimental source: liver
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,Residues: 399-675,'N',677-727 <SEY3>

,Experimental source: liver

;Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.;

Ball, Chem. 266, 5256-5259, 1991

,Title: G to T transversion at position +5 of a splice

,Reference number: ISS349; MUD:91161621; PMID:1672129
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A,Residues: 728-895,'A',897-964 <SEY4>
A,Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the Atlas, December 1977
A;Reference number: A94562
A;Accession: A94562
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A; Molecule type: pro
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A/Accession: S05-212
A/Accession: S05-212
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A/Accession: S05-216
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Alternate names: procollagen alpha 1(III) chain
Abternate names: procollagen alpha 1(III) chain
Bate: 24-Apr-1984 #sequence revision 01-Sep-1995 #text change 09-Jul-2004
Accession: $05272; $04642; PE0011; $01726; $04887; A90399; A94562; I51868; $59511; A90
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A; Residues: 1-170 <TOM>
A; Residues: 1-170 <TOM>
A; Cross-references: EMBL: X07240; NID: g30060; PIDN: CAA30229.1; PID: g30061
A; Cross-references: EMBL: X07240; NID: g30060; PIDN: CAA30229.1; PID: g30061
A; Vaneczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1989
A; Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
A; Reference number: S04887; MUID: 89386015; PMID: 2780304
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GP---RGPAGPIGPPGP---AGQPGDXGEGGSPGLPGIAGPRGGPGERGEHGPPGPAGFP 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 932 GPPGAQGPPGSPGPLGIAGLTGARGLAGPPGMPGPRGSPGPQGIKGESGKPGASGHNGER 991
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Submitted to the EMBL Data Library, February 1989
A;Reference number: S05272
A;Accession: S05272
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F;154-167/Region: amino-terminal nonhelical telopeptide
F;168-1196/Region: helical
F;168-1196/Region: cell attachment (R-G-D) motif
F;1197-1221/Region: cell attachment (R-G-D) motif
F;1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F;123-1466/Domain: carboxyl-terminal propeptide #status predicted cCPR>
F;123-1466/Domain: carboxyl-terminal propeptide #status predicted
F;124/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;151-1212/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental
F;263/Rainding site: carbohydrate (Lys) (covalent) #status experimental
F;584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
F;584,1094/Modified site: Gly-Ile (collagenase) #status experimental
F;1106/Einding site: carbohydrate (Lys) (covalent) #status predicted
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A; Residues: 1165-1196 (EMA>
A; Residues: 1165-1196 (EMA>
A; Residues: 1165-1196 (EMA>
A; Cross-references: GB: MI1134; NID: g180417; PIDN: AAAS2004.1; PID: g180418
B; Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4357-4363, 1985
A; Title: Isolation of CDNA and genomic clones encoding human pro-alphal(III) collagen. B
A; Recession: A92516
A; Rocession: A92516
A; MulD: 85157600; PMID: 2579949
A; Molecule type: DNA
A; Residues: 1176-1240, V, 1242-1356, P, 1358-1466 (CHU)
A; Residues: 1176-1240, V, 1242-1356, P, 
                                                                                                                                                                                                                                                                             A,MOICTIL TITLE TO BE BENEAU

A,MOICTIC TITLE TO BE BENEAU

A,CTOSS-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054

B,CTOSS-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054

B,CSVET, J, M., Kangy, A.H.

B,CSVET, J, M., Kangy, A.H.

B,TITLE: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9 from ty

A,Reference number: A90446; MUID:81208139; PMID:7016180

A,MOICCULE type: protein
A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syn R;Mankoo, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1989
A;Fifle: Human pro alphal(III) collagen: cDNA sequence for the 3' end.
A;Reference number: S02119; MUID:88189827; PMID:3357782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416
R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm A;Reference number: 159025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 2431-2431
A;Introns: 2711: 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Introns: 2711: 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Note: the list of introns is incomplete; defects in this gene can result in Shlers-Dan C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide here of their length, is formed with desmosine cross-links made from lysine and allysine h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL;X01655; EMBL;X01742; NID:g29584; PIDN:CAA25821.1
R;Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant
Bjochemistry 25, 1408-1413, 1986
Bjochemistry 25, 1408-1413, 1986
A;Reference number: Is collagen gene expression is coordinately modulated with the type
A;Reference number: Is 2393; MUID:86187804; PMID:3754462
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F;1-23/Domain: amino-terminal propeptide #status predicted <PRO>
F;31-91/Domain: von Willebrand factor type C repeat homology <VWC>
F;15-4-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: structural component of extracellular fibrous polymer that maintains inte
C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit _3.hydroxylated and some are subsequently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Gene: GDB:COL3A1
A;Cross-references: GDB:118729; OMIM:120180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Residues: 1065-1155,'P',1157-1466 <LOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1161-1200 <MIS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ation
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294 GAPGPMGPRGAPGERGRP---GLPGAAGARGNDGARGSDGQPGPPGPPGTAGFPGSPGAK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 GEVGPAGSFGSNGAPGQRGEPGPQGHAGAQGPPGPPGINGSPGGKGEMGPAGIPGAPGLM 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471 GEPGANGLPGAAGERGAPGFRGPAGPNGIPGEKGPAGERGAPGPAGPRGAAGEPGRDGVP 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GAQGPPGPAGPAGERGEQGPAGSPGFQCLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 GARGPPGPAGANGAPGLRGGAGEPGKNGAKGEPGPRGERGEAGIPGVPGAKGEDGKDGSP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 GKNGERGGPGGPGPPGKNGETGPQGPPGPTGPGGDKGDTGPPGPQGLQGLPGTGGPP 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              651 GENGKPGEPGPKGDAGAPGARGKGDAGAPGERGPPGLAGAPGLRGGAGPPGPEGGKGAA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP-------GPAGPKGSP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 GEAGRP---GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGV- 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              771 GPAGQPGDKGEGGAPGLPGIAGPRGSPGERGETGPPGPAGFPGAPGQNGEPGGKGERGAP 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               559 GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          891 GPPGPSGSPGKDGPPGPAGNTGAPGSPGVSGPKGDAGQPGEKGSPGAQGPPGAPGIA 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         619 GPTGL-----PGPPGERGGPGSRGF-----PGADGVAGPKGPAGERGSPGPAGPKGSP 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GPSGPAGEPGPT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519 --MGFPGPKGAAGEPGKAGERGVPGP--------PGAVGPAGKDGEAGAQ 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                831 GEKGEGGPPGVAGPPGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGARGLPGPPGSNGNP 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           667 GEAGRPGEAGLPGA-----KGLTGSPGSPGPDGKTGPPGP----AGODGRPGPP 711
                                                                                                                                                          -----GADGVAGPKGPAGER 42
                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GPPGPPGARGQAGVMGFPGPK---GAAGEPGKAGERGVPGPPGAVGPA---GKDGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEA
                                                                                                                                                                                                                                                                                                           GSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP-----
51.1%; Score 2370; DB 1; Length 1466;
49.5%; Pred. No. 4.9e-111;
iive 56; Mismatches 285; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 GEAGKPGEOGVPGDLGAP-------
                                                                                                                                                          1 GPPGEPGPTGLPGPPGERGGPGSRGFP----
                                     Best Local Similarity 49.5
Matches 476; Conservative
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Fig91-29-76egion: cell attachment (R-G-D) motif
Fil067-1066/Region: cell attachment (R-G-D) motif
Fil067-1069/Region: cell attachment (R-G-D) motif
Fil067-1069/Region: cell attachment (R-G-D) motif
Fil128-1126/Region: cell attachment (R-G-D) motif
Fil129-1126/Region: cell attachment (R-G-D) motif
Fil21-126/Region: cell attachment (R-G-D) motif
Fil225-126/Region: cell attachment
                                                                                                                                                                                                                                                                   type V procollagen COOH-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: DNA A; Residues: 1449-1465, A, CTSI> A; Residues: 1449-1465, E, 1465-1495, A, CTSI> A; Residues: 1491-1465, E, 1465-1495, A, CTSI> A; Cross-references: GB: 303051, NID: 9179695, PIDN: AAA51858.1; PID: 9179696 A; Cross-translated the codon GAA for residue 1460 as Gln, and GAG for residue C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit are 5-hydroxylated and subsequently O-glycosylated.
C; Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GDB:119064; OMIM:120190
A,Cross-references: GDB:119064; OMIM:120190
A,Map position: 2331-231
A;Introns: 3371; 812/3; 8330
C;Complex: 13571; 812/3; 818/3; 848/3; 902/3; 902/3; 974/3; 1046/3; 1064/3; 1448/3
C;Complex: type V collagen may be a homotrimer of alpha I(V) chains (see PIR:CGHUIV), a labba 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among the ength, is formed with desmosine cross-links made from lysine and allysine residues
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: structural component of extracellular fibrous polymer associated with cell A; Note: may play a role in controlling the lateral growth of collagen I fibrils A; Note: may play a role in controlling the lateral growth of collagen I fibrils C; Superfamily: collagen alpha 1(I) chain; fibrilar collagen carboxyl-terminal homology; C; Keywords: colled coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolli F; 1-26/Domain: signal sequence #status predicted <a href="Missangle-sequence">Missangle-sequence</a> #status predicted <a href="Missangle-sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COL3A1 and COL5A2, located on
                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: mRNA
A) Residues: 1227-1417, T',1419-1437,'S',1439-1496 «MYE>
A) Residues: 1227-1417, T', 1419-1437,'S',1439-1496 «MYE>
A) Experimental source: normal fibroblasts
A) Experimental source: normal fibroblasts
Grandics 3, 275-277, 1988
A) Fisipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, A, Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, locat A, Reference number: A30017; MUID:89138450; PMID:3224983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1250-1251/Cleavage site: Glu-Asp (procollagen C-endopoptidase) #status predicted 17.259,1397/Binding site: carbohydrate (Asn) (covalent) #status predicted F;1293,1299,1325/Disulfide bonds: interchain #status predicted F;1333-1494,1402-1447/Disulfide bonds: #status predicted
                              A;Cross-references: GB:MI1135; NID:g179693; PIDN:AAA51857.1; PID:g179694 A;Note: part of this sequence were determined by protein sequencing R;Myers, J.C.; Loidl, H.R.; Seyer, J.M.; Dion, A.S. J. Biol. Chem. 260, 11216-11222, 1985
A;Title: Complete primary structure of the human alpha-2 type V procollace. A;Reference number: A25374; MUID:85289337; PMID:2411731
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48.2%; Pred. No. 7.6e-109;
ive 52; Mismatches 287;
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Matches 478;
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                                                                                                                                                                               GPPGARGQAGVMGFPGPKGAAGEPGKAGERGV-----PGPPGAVGPAGKDGEAGAQ
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A; Residues: 1003-1034 <RES>
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Qy 640 GADGVAGPKGPAGERGSPGPAGPKGSPGEJ	C; Decases: 02-011-1996 #sequence_revision 02-011-1996 #text_change 09-011-2004 C: Accession: 149607
	14950/ procollagen type V alpha 2 - mouse Consories Mus musculus (house mouse)
Qy 586 GPAGP PGEAGKPGEQGVPGDLGAI	RESULT 14
Db 895 GGRGTQGPPGATGFPGSAGRVGPPGPAGAL	Db 1194 GPPGVRGSVGEAGFEGPPGFPGPPGPPG 1224
Qy 541GPPGAVGPAGKDGEAGACGPI	793 GPPGEAGKPGEQGVPGDLGAPGPSGPAG
DD 835 GENGPTGAVGFAGPQGSDGQPGVKGEPGEI	1134 GDRGQKGHRGFTGLQC
Qy 496GPAGQDGREGPPGAFG	747PGAVGPAGKDGBAGAQGPPGPAGBRGEQGPAGSPGFQGLPGPA
	1074 GLPGSQGAPGTPGPVGAPGDAGQRGDPGSRGPIGHLGRAGKRGLPGPQGPRGDKGDHGDR
Qy 448 GERGSPGPAGPKGSPGEAGRPGEAGLE	GODGRPGPPGPPGARGOAGWGFPGPKGAAGEPGKAGBRGVPGP
Db 715 GERGEPGITGLPGEKGMAGGHGPDGPKGNE	GKVGPTGATGDKGPPGPVGPPGSNGPVGEPGPBGPAGNDGTPGRDGAVGERGDRGDPGPA
Qy 411AGEPGPTGLPGPPGERGG	643 GVAGPKGPAGERGSPGPAGPKGSPGEAGLPGEAGLPGAKGLTGSPGSPGFDGKTGPPFGPA
358	0-
20 00	Db 894 GGRGTQGPPGATGFPGSAGRVGPPGPAGAPGPAGFPGEPGKEGPPGPRGDPGSHGRVGVR 953
0 0	Qy 541GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLP 585
Qy 238 GPKGPAGERGSPGPAGPKGSPGEAGRPGEA 1	GENGPTGAVGFAGPQGSDGQPGVKGEPGEPGQKGDAGSPGPGPGGAGSPGPHGPNGVPGLK
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QY 181 GPPGEAGKPGEQGVPGDLGAPGPSGPA	
Db 415 GLPGAVGTDGTPGRKGATGSAGTSGPPGLA	PGPKGDR
Qy 121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAC	45
355	DD 657 GLRGERGEQGPPGPPGPPGPPGBPGRPGDQGVPGGPGAVGPLGPRGERGNPGER 716
TO GENERAL POLICE CONTROLLED OF THE PROPERTY O	Qy 361 GPAGERGEGGPAGSPGFQGLPGPAGPPGEAGKPGEGGVPGDLGAPGPSGPA 411
	Db 597 GPPGSIGIKGQPGTMGLPGPKGSNGDPGKPGPGQPGGPGRADGRVGPYGPPGPP 656
Db 235 GPPGEPGEPGPMGPIGSRGPEGPPGKPGED	537 GAQGERGPVGSSGPKGSQGDPGRPGEPGLFGARGLTGNPGVQGPEGKLGPLGAPGEDGRP
Qy 1 GPPGEPGPTGLPGPPGE-	
Query Match Query Match Best Local Similarity 47.6%; Pred. No. Matches 473: Conservetive 55; Mismatc	
F;1270-1497/Domain: fibrillar collagen carbo	OV 181 GPPGEAGKPGEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK 240
A,Gene: Colsa-2 C,Superfamily: collagen alpha 1(I) chain; fi F;39-98/Domain: von Willebrand factor type C	Oy 121 GEPGKAGERGEPGAVGPPGGAOGPPGPAGGAGAGGGGGGGAGAGGGGGGGGGG
A; Cross references: UNIPROT: Q61431; GB: L0291 C; Genetics:	Db 357 GAHGMPGKPGFMGPLGIPGSSGFPGNPGMKGEAGPTGARGPEGPQGQRCETGPPGPVGSP 416
A;Status: greinmining; crambiated itch of ma A;Molecule type: mRNA A:Decidine: 1-1407 / PPE;	Qy 70 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGPPGPKGAA 120
A, Reference number: 149607; MUID:93214071; F	297 GLKGHRGHKGLEGPKGEVGAPGSKGEAGPTGPMGAMGPLGPRGMPGERGRLGPQGAPGQR
A.mitlacopouros, A.; Guzunt, A.; Corres, Dev. Dyn. 195, 113-120, 195, The A.mitlacopourostion of pro-alpha 2(V) coll	OXGCFEGFFGFFGEFGFFGFFGFFGFFGFFGFFGFFGFFGFFGF
R. Andrikopoulos, K.; Suzuki, H.R.; Solursh,	737

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318; NID: 9309180; PIDN: AAA37440.1; PID: 930918
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                       lagen transcripts in the tissues of the deve PMID:1297453
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. 9.9e-108;
. ches 289; Indels 177; Gaps
M.; Ramirez, F.
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Qy 277 GSPGSPGKTGPPGPAGQDGRPGPPGARGOAGWGFPGPKGAAGEPGKAGERGVP 336 bb 460 GSPGNVGPSGPFGLPGLDGRPGPFGPAGPGPGPGPGPGRGHP 519 CQ 337 GPPGAVGPAGKDGAGAGPAGERGEGGPAGSPGPGCPGCAGPGPGPGB 519 QY 337 GPPGAVGPAGKDGAGAGERGEGGPAGSPGPGCPGCAGPGCPGCAGPGCPGBG 396 Db 520 GLAGARGAPGPDGNCGAGPGCQCQGCGGBCGPAGPFGCLPGPSGTTGSVGKPGER 579 QY 397 GVPGDLGAPGPSGPAGEPGCQCQGCGGBCGPAGPFGCLPGPSGTTGSVGKPGER 579 CQ 397 GVPGDLGAPGPSGPAGEP	00 040 GASGPGGLPGERGAGIPGGKGEKGETGLRGDTGNTGRDGARGIPGAVGAPGFAGASGDR	595 874 652 931 712	Qy 763 GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820			
Db 1012 GTPGKVGPTGATGDKGPPGPVGPPGSNGPVGEPGPBGDAGNDGTPGRDGAVGERGDRGDP 1071	RESULT 15 A43291 collagen alpha 2(I) chain precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: A43291; A54328 R;Phillips, C.L.; Morgan, A.L.; Lever, L.W.; Wenstrup, R.J. G;Accession: A43291; A54328 A;Title: Sequence analysis of a full-length cDNA for the murine pro alpha 2(I) collagen A;Reference number: A43291; MUDD:92372043; PMID:1505972 A;Reference number: A43291; MUD:92372043; PMID:1505972 A;Status: preliminary; not compared with conceptual translation	Aprolecule type: mRNA A; Molecule type: mRNA A; MRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule typ	A,Gene: COL1A2 C,Superfamily: collagen alpha 2(1) chain; fibrillar collagen carboxyl-terminal homology C;Superfamily: coiled coil; extracellular marrix; glycoprotein; trimer; triple helix C;Keywords: coiled coil; extracellular marrix; glycoprotein; trimer; triple helix F;1145-1373/Domain: fibrillar collagen carboxyl-terminal homology <fcc> Query Match Query Match 49.6%; Score 2300, DB 1; Length 1373; Best Local Similarity 47.4%; Pred, No. 1.40-107; Matches 483; Conservative 50; Mismatches 275; Indels 210; Gaps 20;</fcc>	QY 1 GPPGEPGPTGLPCPPGERGFPGADGVAGPKGPRGERGSPGPAGPKGSPGEAGRP 60 Db 103 GPRGPPGAVGAPGPGSPGEPGGPGEPGGTGPAGPRGPAGSPGKAGEDGHPGKPGRP 159 QY 61 GEAGLPGAKGLTGSPGSP	QY 109 GWAGFPGBKGAAGERGVPGPPGAVGPAGKDGEAGAQGPP 153 D 220 GARGLPGBRGRVGAPGARGSDGSVGPVGPAGPIGSAGPPGFPGAPGPKGBLGPVGNP 279 QY 154 GPAGPAGBRGEQGPAGSPGPQGL	Qy 181

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October 18, 2004, 13:23:10 ; Search time 146.729 Seconds (without alignments) 3219.411 Million cell updates/sec
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4640
1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 821
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                               OM protein - protein search, using sw model
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Sequence:
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1825181 Total number of hits satisfying chosen parameters:

1825181 segs, 575374646 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAH63249	0601J5	AAR24536	Q9W7R9	O6P4Z2	AAH63191	Q91717	07ZTI6	Q6PEI9	AAH58045	991718	Q7ZTM4	Q6NZ15	AAH66384	
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ALIGNMENTS

RESULT 1

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Bernard

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Barsh G.S., Roush C.L., Bonadio J., Byers P.H., Gelinas R.E.,
"Intron-mediated recombination may cause a deletion in an alpha 1 type
I collagen chain in a lethal form of osteogenesis imperfecta.";
Proc. Natl. Acad. Sci. U.S.A. 82:2870-2874 [1985].
                                                                                                                                                                                                                                                                     SEQUENCE OF 1179-1464 FROM N.A., VARIANTS OI-II HIS-1277; ARG-1388 AND 1337-GLU-TYR-1338 DEL, AND VARIANT SER-1434.

MEDLINE-933552646; PubMed=834569; P.H.;

Chesslar S.D., Wallis G.A., Byers P.H.;

"Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of type I collagen result in defective chain association and produce lethal osteogenesis imperfecta.";

J. Biol. Chem. 268:18218-18225(1993).
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transcriptional
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Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
"A comparative study of glycopeptides derived from selected vertebrate
            Prockop D.J.;
"Nucleotide sequences of complementary deoxyribonucleic acids for the pro alpha 1 chain of human type I procellagen. Statistical evaluation of structures that are conserved during evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-34 FROM N.A.
MEDLINE=85130970; PubMed=2857713;
Chu M.-L., de Wet W. W., Bernard M.P., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
Promoter structure, Alul repeats, and polymorphic transcripts.";
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                                                                                         SEQUENCE OF 472-607 FROM N.A.
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1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPG 1190

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MEDLINE=91374476; PubMed=1895312;

REVIEW ON OI VARIANTS

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Homo sapiens (Human)
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Mammalia; Eutheria;
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Length 1464;
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 Score 2765; DB.1;
Pred. No. 2.6e-103;
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31; Mismatches
 59.6%;
                  Best Local Similarity 55.4
Matches 561; Conservative
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MEDIJINE-899025644; PubMed-3178743;
Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
Jaenisch R., Prockop D.J.;
"Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
of human type I procollagen.";
Biochem. J. 253:919-922(1988).
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; APO17178; AAB94054.2; -.
GO; GO:0005737; C:collagen; IEA.
GO; GO:0005737; C:cytoplagn; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
GO; GO:0006817; P:extracellular matrix
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MEDLINE=85130970; PubMed=2857713;
Chu M.L., de Wet W., Bernard M., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (1) collagen
Promoter structure, Alul repeats, and polymorphic transcripts.";
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Gene 67:105-115(1988).
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tko i., De Paepe A., Nuytinck i., Barley J.,
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Primates, Catarrhini, Hominidae,
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Last sequence update)
Last annotation update)
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Highly conserved sequences in the 3'-untranslated
COLIA1 gene bind cell-specific nuclear proteins.";
FESS Lett. 279:9-13(1991).
                                                                  PRT;
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                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26, Pro alpha 1(1) collagen.
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MEDLINE=98107942; Pubmed=
Korkko J., Ala-Kokko L.,
Prockop D.J.;
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.larity 55.3%; Pred. No. 3.8e-103;
Conservative 31; Mismatches 229;
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR001007; VWP_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD002079; Fib_collagen_C; ProDom; P000007; Clg_helix; 3.
ProDom; P0002079; Fib_collagen_C; 1.
SWART; SW00214; VWC; 1.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS50184; VWFC 1; 1.
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Altschul S.F., Zeeberg B.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Bottchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hales S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP 1015
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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TISSUBErain:
Strausberg W.
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 25, Last annotation update)
Alpha 1 type I collagen, preproprotein.
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                                                                    Gaps
                                                                   Indels 192;
                                               Length 1464;
                             1464 AA; 139010 MW; B0581F8D1C89DDE8 CRC64;
                                               ; Score 2761; DB 2;
; Pred. No. 3.8e-103;
31; Mismatches 229;
                                                                                                                                                                                                                                                    GPPGEAGKPGEQGVPGDLGAP----
                                                Query Match
Best Local Similarity 55.3%;
Matches 560; Conservative 3:
 PS501208; VWFC 1; 1. PS50184; VWFC 2; 1.
                     Collagen.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                 274
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 PROSITE;
PROSITE;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campbell B.G., Wootton J.A.M., MacLecd J.N., Minor R.R.; "Sequence of normal canine COLIA1 cDNA and identification of a heterozygous alphal(I) collagen Gly208Ala mutation in a severe case of canine osteogenesis imperfecta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arch. Blochem. Blophys. 384:37-46(2000).

-!- FUNCTION: Type I collagen is a member of group I collagen

-(fibrillar forming collagen).

-(SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

-!- PTM: Prolines at the third position of the tripeptide repeating

unit (G-X-Y) are hydroxylated in some or all of the chains.

-!- DISEASE: Defects in COLIA1 are a cause of osteogenesis imperfecta

(OI).
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                                                                                                                                                                                                                                                                                                                                30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-MAY-2004 (Rel. 45, Last annotation update)
Collogen alpha 1(1) chain precursor.
Name=COLLAl;
Canis familiaris (Dog).
Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                             1139 GPRGPPGSAGAPGKDGLNGLPGPPGPRGRTGDAGPVGPPGPPGPPG
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Triple-helical region.
Nonhelical region (C-terminal).
Cell attachment site (Potential)
Cell attachment site (Potential)
Pyrrolidone carboxylic acid (By
GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sımılarıty).
Allysine (By similarity).
5-hydroxylysine (By similarity)
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-!- SIMILARITY: Contains 1 VWFC domain.
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Collagen alpha 1(I) chain.
C-terminal propeptide.
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TISSUE=Skin;
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InterPro; IPR008160; Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR001007; VWF_C.
Pfam; PF01391; Collagen. 18.
Probom; PP01391; Collagen; 18.
Probom; PD002078; Fib_collagen_C; I.
Probom; PS001007; VWF_C.
Probom; PS01018; Collagen; 18.
Probom; PS01018; Fib_collagen_C; 1.
PROSITE; PS01028; VWFC_Z; 1.
PROSITE; PS01084; VWFC_Z; 1.
Collagen; Connective Lissue; Disease much and a collagen; Connective Lissue; Disease much a collagen; Pytrolidor collagen;
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                                                                                                                                                                                                                                                                                                                           STANDARD;
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190 GEQGVPGDLGAP------
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                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 556; Conserv
                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                          247 GARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLPGER 306
                                                                                                                                                                                                                               148 GAQGPPGPAGPAGERGEQGP------AGSPGFQGLPGPAGPPGEAGKPGEQ 192
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                                                                                              Gaps
50 3-hydroxyproline (By similarity).
51 0-linked (Gal. .) (By similarity).
51 N-linked (GloNAc. .) (By similarity).
63 G -> A (in OI; severe).
64 138762 MW; 58E3674D2B570697 CRC64;
                                                                                             Indels 180;
                                                                      Length 1460;
                                                                     59.5%; Score 2759; DB 1; 55.9%; Pred. No. 4.5e-103; ive 31; Mismatches 230;
                                                                                              Conservative
             261
1361
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                                    208 20
1460 AA;
                                                                                   Similarity
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                                                                                  Best Local Simi
Matches 559;
 MOD RES
CARBOHYD
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---GPSGPA------GEPGPTGLPGPPGER 222
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MEDINE=99153824; PubMed=10065941;
Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
"Expression of collagen alphal(I) mRNA variants during tooth and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 GPPGQDGIPGQPGLPGPPGPPGPLGLGGNFASQMSYGYDEKSAGVSVPGPMGPSGPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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J. Dent. Res. 78:11-19(1999).

EMBL: 7/8279; CABOLO53.1;
GO; GO:0005581; C:collagen; IEA.
GO; GO:0005517; C:cytoplasm; IEA.
GO; GO:0006517; P:phosphate transport; IEA.
InterPro; IPRO08161; Clg helix.
InterPro; IPRO08161; Clg helix.
InterPro; IPRO08165; Fib.collagen.
InterPro; IPRO09041; PMP_SGCI.
InterPro; IPRO09041; PMP_SGCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137886 MW; E6896BDC19A4A1D8 CRC64;
                                     1147 GKDGLNGLPGPPGPPGRRTGDAGPVGPPGPPGPPG 1186
   820
                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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Probom, PD000007; CIG helix; 3.
SMART, SM0018; Coller; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01,
01-JUN-1998 (TrEMBLrel. 06,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF01410; COLFI; 1.
Pfam, PF01391; Collagen; 18
                                                                                                                                                                                                                                                                                                                                                                                             Collagen alphal (Fragment).
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19;

176

42

236

99

us-10-658-989a-3.rup

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SEQUENCE OF 518-1128 FROM N.A.
MEDLINE-86137-0431, Pubmed=3841523;
MEDLINE-86137-0431, Pubmed=3841523;
"Nucleotide sequence of a cDNA clone for mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR: S57243; S21626.
MGD; MGI: 88467; Collal.
InterPro; IPR000161; Collagen.
InterPro; IPR000160; Collagen.
InterPro; IPR000160; WPF_CCI
InterPro; IPR0001001; WPF_GCI.
InterPro; IPR0001007; WPF_CC.
Pfam; PF01410; Collagen; 18.
ProDom; PD000007; CIQ helix; 1.
ProDom; PD000007; CIQ helix; 1.
ProDom; PS0000778; Fib_collagen_C; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMEL, U08020, AAA88912.1; EMEL, U08020, AAA88912.1; EMEL, M14423, AAA37333.1; EMEL, M14423, AAA37333.1; EMEL, M07053, CAA29927.1; EMEL, K03036, AAA37332.1; CAA37032.1; EMEL, K03030, AAA37332.1; JOINED. EMEL, K03031, AAA37332.1; JOINED. EMEL, K03032, AAA37332.1; JOINED. EMEL, K03033, AAA37332.1; JOINED. EMEL, K03033, AAA37332.1; JOINED. EMEL, K03034, AAA37332.1; JOINED. EMEL, K03034, AAA37332.1; JOINED. EMEL, K03035, AAA37332.1; JOINED.
                                                                                                                                                                                                                                                                  Mol. Cell. Biol. 2:1362-1371(1982)
                                                                                                                                                                 SEQUENCE OF 735-1130 FROM N.A.
                                                                                                                       Gene 39:311-312(1985).
  1136
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                                                                                        GGPGSRGFPGADGVAGPKGPSGERGSPGPAGPKGSPGBAGRPGEAGLPGAKGLTGSPGSP
                                                                                                                                               GPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAV
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CA11087; 056635;
01-JUL-1989 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last amnotation update)
01-OCT-2004 (Rel. 45, Last amnotation update)
Collagen alpha 1(1) chain precursor.

Name=Colla1; Synonyms=Cola1;
Name=Colla1; Synonyms=Cola1;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Li S.W., Khillan J., Prockop D.J.;
"The complete cDNA coding sequence for the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i I procollagen.";
Biol. 14:593-595(1995)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
collagen
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-!- SIMILARITY: Belongs to the fibrillar collagen family.
-!- SIMILARITY: Contains I VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            procollagen gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
MEDLINE=83157109; PubMed=6219867;
Monson J.M., McCarthy B.J.;
Midentification of a Balb/c mouse pro alpha 1(1) procollagen gene:
evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
pro alpha 1(I)
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=83141374; PubMed=6298597; McCarthy B.J.; Mc
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                      Procollagen, type I, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                        ------RGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48
                                                                                                                                                                                                                                                                                                                                                GPKGSPGEAGRP------GEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQD 93
                                                                                                                                    Allysine (By similarity).
5-hydroxylysine (By similarity).
3-hydroxyproline (By similarity).
N-linked (GloNAc. .) (Potential).
O-linked (GloNAc. .) (By similarity).
N-linked (GloNAc. .) (By similarity).
Cell attachment site (Potential).
A -> V (in Ref. s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA
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                                                                                                                                                                                                                                                                                   Gaps
                     e, Extracellular matrix, Glycoprotein; carboxylic acid, Repeat, Signal.
                                                                                                                                                                                                                                                               DB 1; Length 1453;
                                                                                                                                                                                                                                                                                   Mismatches 240; Indels 180;
                                                                                          Nonhelical region (N-terminal).
Triple-helical region.
Nonhelical region (C-terminal).
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                 . V (in Ref. 5).
3B802E535DF81808 CRC64;
                                                   N-terminal propeptide.
Collagen alpha 1(I) chain.
C-terminal propeptide.
                                                                                                                                                                                                                                                            Score 2732.5; DB 1
Pred. No. 5:2e-102;
                                                                                                                                                                                                                                           137944 MW;
                                                                                                                                                                                                                                                                                   33;
PROSITE; PS01208; WWFC_1; 1.
PROSITE; PS50184; WWFC_2; 1.
Collagen; Connective tissue;
Hydroxylation; Pyrrolidone ca
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.7%;
Matches 547; Conservative 3
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MGD, MGI:88467; Collal.
GO, GO:0005581; C:cytoplagen; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
GO; GO:0006817; P:extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
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Best Local Similarity 58.49
Matches 524, Conservative
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                                                                                                                                                                                                                                                                                  Collagen.
SEQUENCE 1453 AA; 138032 MW; 0B7F06BBB9AlD5EA CRC64;
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR008041; PMP_Collagen_C.
InterPro; IPR001007; VWF_C.
Ffam; PF01410; CoLFF; 1.
Pfam; PF01391; Collagen; 18.
Pfonom; PD000007; Clg helix; 3.
ProDom; PD000007; Clg helix; 3.
ProDom; PD002078; Pib_collagen_C; 1.
SWART; SW00214; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
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GGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEAGLPGAKGLTGSP
                                                                                                                              GSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1069;
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S. EMBL, X99705, TOTA CASO TO THE EMBL/GenBank/DDBJ databases.

EMBL, X99705, D897041.1; -...

R INTERPROFILE OF GOLINGEN.

R INTERPROFILE OF COLINGEN.

R PÉRM: PPO01391, COLINGEN.

R PÉRM: PPO01391, VWC; 1.

R PROSITE; PS01208, VWC; 1.

R PROSITE; PS01208, VWFC_1; 1.

R PROSITE; PS01208, VWFC_1; 1.
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1069 AA; 97445 MW; EE279B10572FB980 CRC64;
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27, Last sequence update)
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EE279B10572FB980

97446 MW;

1069 AA;

SEQUENCE

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GAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGERGPPGPMGPP 1003
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Catarrhini; Hominidae; Homo.
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CA67261,
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JT 02-MAR-2004 (Trembirel 27, Last sequence update)
JT 02-MAR-2004 (Trembirel 27, Last annotation update)
DT 02-MAR-2004 (Trembirel 27, Last annotation update)
DE Collagen type I alpha I (Fragment).
GN COLLAI.
GN COLLAI.
GN Edwaryots, Metazoa; Chordata, Craniata, Vertebrata; E.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                117;
 2; Length 1069;
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Query Match 57.8%; Score 2681.5; DB 2; Best Local Similarity 58.4%; Pred. No. 4.6e-100; Matches 524; Conservative 28; Mismatches 229;
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(Rel. 12, Last sequence update)
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Simon M., Pedettour F., O'Brien K., Sirvent N., Kedra D., Guilbaud C Turc-Carel C., Dumanski J.P.;
"Regulation of the platelet-derived growth factor B-chain gene via fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans and giant-cell fibroblastoma.";
BMBL, Genet. 15:95-98(1997).
BMBL, SAS705; CAA67261.1; -.

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GPPGEPGPTGLPGPPGERGCPGSRGFPGADGVAGPKGPA
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send an email to license@isb-sib.ch)
                                                         EMBL; V00401; CAA23665.1; -...
EMBL; M10571; AAA48671.1; -...
EMBL; M10571; AAA48672.1; -...
EMBL; M27179; AA748672.1; -...
PIR; 150629; 150629.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Collagen.
InterPro; IPR001007; VWF_C.
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Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
                              EMBL; M17839; AAA48704.1; -.
EMBL; M17838; AAA48704.1; JOINED.
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Pfam; PF01391; Collagen; 18.
Pfam; PF00093; VWC; 1.
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                                                                                                                                                                                                                                                                                                                                                                               MEDINE-82231995; PubMed=7093229; 'NEDINE-82231995; PubMed=7093229; 'NEDINE-8EZ331995; PubMed=7093229; 'NEDINE-8EZ331995; Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H., Gross J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1200-1205.
MEDLINE-72243016; PubMed=5047697;
Eyre D.R., Glimcher M.J.;
"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";
Biochem. Biophys. Res. Commun. 48:720-726(1972).
                                                              Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-81160715; PubMed-6927845; Fuller F., Boedtker H.; "Sequence determination and analysis of the 3' region of chicken proappna 1(I) and pro-alpha 2(I) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences."; Biochemistry 20:996-1006(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                              "Amino acid sequence of chick skin collagen alpha 1(I)-CB8 and the complete primary structure of the helical portion of the chick skin collagen alpha 1(I) chain."; Blochemistry 21:2048-2255(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=80134546; PubMed=6987088; MEDLINE=80134546; PubMed=6987088; Pabwalter A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T., Pastan I., Decrombrugghe B., Feitzek P.P., Olsen B.R.; "Nucleotide sequence of a collagen cDNA-fragment coding for the carboxyl end of pro alpha 1(I)-chains."; FEBS Lett. 11:61-66(1980).

-!- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).

-!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                    SEQUENCE OF 1-144 FROM N.A.

MEDLINE=88007542; PubMed=2820966;
Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Aho S., Gerstenfeld L.C., Boedtker region and the first introm of the chicken pro-alpha 1(1) collagen gene.";
J. Biol. Chem. 262:13323-13322(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTW: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X. SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                      Finer M.H.; Boedtker H., Doty P.; "Construction and characterization of cDNA clones encoding the control pro alpha 1(I) collagen mRNA."; Gene 56:71-78(1987)
                Collagen alpha 1(I) chain precursor
                                                                                                                                                         MEDLINE=88056316; PubMed=3678834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 981-1453 FROM N.A.
                                                                                                                                          SEQUENCE OF 1-153 FROM N.A.
                                             Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 152-1187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hydroxyapatite.
                                                                                                             NCBI_TaxID=9031;
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GSPGPDGKTGPPGPAGDGRPGPPGPRGAGWGFPGPKGAAGBPGKAGERGVPGPP 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKDGEAGAQGPPGPAGPAGERGEQGP-----AGSPGFQGLPGPAGPPGEA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 GAPGPKGNSGEPGAPGNKGDTGAKGEPGPAGVOGPPGPAGEEGKRGARGEPGPAGLPGPA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 GLPGERGRPGPSGPAGARGNDGAPGAPGPPGPTGPAGPPGFPGAAGAKGETGPQGARGSE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GRPGPPGPPGARGQ---AGVMGFPGPKGAAGE---PGKAGERGVPGPPGAVGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1153 1153 3-hydroxyptoline.
254 254 0-linked (Gal. . .) (By similarity).
1354 1354 N-linked (Gal. . .) (By similarity).
1187 1187 F - L (in Ref. 5).
1441 1441 Q - H (in Ref. 6).
1453 AA; 137789 MW; 3BC6152134271F4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 7e-100;
30; Mismatches 250; Indels 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; DB 1; Length 1453;
7e-100;
                                                                                                                                                                                                                                                                                                                                                            Allysine (By similarity).
5-hydroxylysine (By similarity)
5-hydroxylysine (Potential).
Hydroxyproline (Potential).
5-hydroxylysine (Potential).
                                                                                                                                                                                                                                                                                                                                Pyrrolidone carboxylic acid.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
Collagen, Connective tissue; Direct protein sequencing;
Extracellular matrix; Glycoprotein; Hydroxylation;
Pyrrolidone carboxylic acid; Repeat; Signal.
1 22
                                                                                                                                                                                                                                   chain
                                                                                                                                                                                             N-terminal propeptide.
Collagen alpha 1(I) ch
C-terminal propeptide.
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Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .074 GPAGPQGPRGDKGETGEQGDRGMKGHRGFSGLQGPPGPPGAPGEQGPSGASGPAGFRGPP 1133
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X MEDLINE-92294154; Pubmed=10367734;

Asahina K., Utoh R., Obara M., Yoshizato K.;

Asahina K., Utoh R., Obara M., Yoshizato K.;

Asahina K., Utoh R., Obara M., Yoshizato K.;

T "Cell-type specific and thyroid hormone-dependent expression of genes

T "Cell-type specific and thyroid hormone-dependent expression of genes

T of al (1) and a2(1) collagen in intestine duting

amphibiammetamorphosis."

Matrix Biol. 18 89-103(199).

R Matrix Biol. 18 89-103(1999).

R GO; GO:0005201; EAA390281; F.

R GO; GO:0005201; F. extracellular matrix structural constituent; IEA.

R GO; GO:000617; P:phosphate transport; IEA.

R InterPro; IPR0008160; Collagen.

R InterPro; IPR0008160; Collagen.

R InterPro; IPR000895; Fib collagen.

R InterPro; IPR001007; VWF_C.
                                                                                                                               471
                                                                                                                                             GPPGARGQAGVMGFPGPPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPA 567
                                                                                                                                                                                                                                                       834 GPTGAPGPAGZVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSGNIGLPGPPAGKZ 893
                                                                                                                                                                                                                                                                                                                953
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                          GAVGPAGKDGEAGAQGPPGPAGPAGFRGEQGPAGSPGFOGLPGPAGPPGEAGKPGEOGVP 399
                                                                                                     654 GNAGAPGPAGARGERGFPGERGVQGPPGPQPRGANGAPGNDGAKGDAGAPGAPGNEGPP 713
                                                                                                                                                                                 -----GQDGRPGPP 507
                                                                                                                                                                                                                                                                                       GE---RGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLP 624
                                                                                                                                                                                                                                                                                                                                         GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEAGLPGAK 681
GSPGPDGKTGPPGPAGDGRPGPAGPPGARGQAGVMGFPGPKGAAGEPGKPGERGAPGPP
                                         GDLGAPGPSGPAGE-----PGP----PGP-----TGLPGPPGERGGP
                                                                                                                            -----GEA
                                                                                                                                                                                                                                                                                                                GSKGPRGETGPAGRPGEPGPAGPPGPRGSPGADGPIGAPGTPGPQGIAGQRGVVGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha 1 type I collagen.
Name-alpha 1 type I collagen;
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa; Ghordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSAGAAGKDGLNGLPGPPGPPGPRGRTGEVGPVGPPGPPGPPG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEOGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               -------AGAQGPP--
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GSPGSEGSPGRDGSAGPKGDRGESGPAGPPGAPGAPGAPGPAGPAGPAGKNGDRGETGPAGPA 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGARGQAGVMGFPGPKGAAGEPGKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAPGPOGPGGSPGPKGNNGEPGAQGNKGEPGAKGESGPAGSQGPPGPPGEEGKRGSRGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 GPSGPPGPAGERGAPGSRGFPGADGAGGPKGPPGERGPVGSAGPKGSPGESGRPGEPGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641 GKPGEQGAPGDVGPSGPAGSRGERGFPGERGAIGPPGPQGPRGANGAPGNDGAKGEAGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 -----GPTGLPGPPGERG------GP-GSRGFPGADGV---AGPKGPAGER
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                          144;
                                                                                                                                                                                                                                                Length 1445;
                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         GSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGP-
                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                    F59BB550C9873F04
                                                                                                                                                                                                                                              55.3%; Score 2568; DB 2; 33.6%; Pred. No. 1.9e-95; ive 43; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GARGOAGVMGFPGPKGAAGEPGKAGERG-
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Clg_helix; 4.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM0038; COLFI; 1.
ROSITE; PS01208; VWFC_I; 1.
PROSITE; PS50184; VWFC_Z; 1.
                                                                                                                                                                                                       1445 AA; 137251 MW;
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                                                                                                                                                                                                                                                                   Best Local Similarity 53.6
Matches 516; Conservative
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728

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1089 GERGMKGHRĞFNGMQGPPGPPGSSGEQGAPGPSGPAGPPGSSGSGTGKDGVNGLPGPI 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dPAGPPGPSGEKGSPGSDGPAGAPGIPGPQGIAGQRGVVGLPGQRGERGFSGLPGPAGEP 968
GEPGAKGEPGPAGVQGPPGPSGEEGKRGSRGEPGPAGPPGPAGERGGPGSRGFPGSDGAS 488
                                                                                                                                   GRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357
                                                                                                                                                                                                                                                                  609 GPSGPSGERGEQGPAGSPGFQGLPGSPGPAGEAGKPGEQGAPGDAGGPGPSGPRGERGFP 668
                                                                                                                                                                                                                                                                                                                                                                                                        ------GPAGPKGPAGPKGPAGERGSP------GPAGPKGSPGEAGRP 468
                                                                                                                                                                                                                                                                                                                                                                                                                                GKQGPSGPNGERGPPGPSGPPGLGGPPGEPGREGSPGSEGAPGRDGSPGPKGDRGENGPS
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                                             GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD
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MEDLINE=22388257, PubMed=12477932,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Collal-prov protein.
Xenopus laevis (African clawed frog).
Xenopus laevis (African Clawed frog).
Amphibia: Batrachia: Anura; Mesobatrachia: Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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CTISQUERCE REQUIRED AND A. CORTINDS;

CTISQUERCE REQUIRED AND A. CORTINDS;

MEDLINE=99407244; PubMed=10474166;

MEDLINE=99407244; PubMed=10474166;

Asahina K., Obera M., Yoshizato K.;

Asahina K., Obera M., Yoshizato K.;

REXPESSION Of genes of type I and type II collagen in the formation of evelopment of the blastema of regenerating newt limb.";

Dev. Dyn. 216:59-71(1999).

REMBI, AB01548; BAA3693.1; -..

ROY GO:0005581; C:cytoplagen; IEA.

GO: GO:0005737; C:cytoplagen; IEA.

GO: GO:0005737; C:cytoplagen; IEA.

ROY GO:0006817; P:phosphate transport; IEA.

INTERPRO; IPRO08161; Ciglaelix.

INTERPRO; IPRO08161; Collagen.

RITHERPO; IPRO08161; Collagen.

RITHERPO; EPRO01007; VWF_C.

INTERPRO; PEPOLO COLLAGEN.

REPROMO COLLAGEN: 1.

PERMI: PEPOLO COLLE!: 1.

PERMI: PEPOLO COLLE!: 1.

PERMI: PEPOLO COLLAGEN: 1.

REPRODOM: PRO00007; CIg_helix; 4.

REPRODOM: PRO00007; CIg_helix; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha I type I collagen.
Cynops pyrthngart.
                                                  GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGE-
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SMART; SM00214; VWC; 1
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                                                                                                                                                                                                     391 GKPGEQGVPGDLGAPGPSGPAGE---PGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPA
                                                                                                                                                                                                                                                                                                                        448 GERGSPGPAGPKGSPGEAGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQD
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                                                                                                                                                            GERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEA
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Gepcl3;
Ge-UGL-2004 (TEMBLFel. 27
05-UUL-2004 (TEMBLFel. 27
05-UUL-2004 (TEMBLFel. 27
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SEQUENCE FROM N.A.
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malak M.J., Gunaetne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

B Chill EMBL/GenBank/DDBJ databases.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22341112; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.
Richardson P.;
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54.6%; Pred. No. 6.7e-94;
ive 53; Mismatches 261; Indels 102;
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                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PROSITE; PS50184; VWFC_2; 1.
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TISSUB-Mammary tumor. WAP-TGF alpha model. 7 months old;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T. Moore T. Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuvik S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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27, Last sequence update)
27, Last annotation update)
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869

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CETRAIN-GSTBL/60; TISSUE-Mammary tumor;

RX

NEDLINE=22388257; PubMed=12477932;

RA

RIAUSERE R.D., Feligold E.A., Grouse L.H., Derge J.G.,

RIAUSHORE R.D., Collins F.S., Hagner L., Schaefer C.F., Bhat N.K.,

RA

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA

Batchenko L., Marusina K.A., Rubin G.M., Hong L.,

RA

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA

Richards S., McHan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

RA

Richards S., Worley K.C., Hale S., Carria A.M., Gay L.J., Hulyk S.W.,

RA

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA

Rabersley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA

Minting M.J., Marra M.A.;

RA

Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                              630 GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGNN 689
                                                                                                                                                                                                                                                                                                         750 GARGLIGPIGPPGPAGAPGDKGBAGPSGPPGPIGARGAPGDRGBAGPPGPAGFAGPPGAP 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                      870 GHRGFSGLÓGPPGSPGSPGEQGPSGASGPAGPRGPPGSAGSPGKDGLNGLPGPIGPPGPR 929
GPPGPXGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP
                                                                                                                                                                                                                                 690 GAPGNDGAKGDIGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDAGPKGADGSPGKD
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                                                                             GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP-----
                                                                                                                                                                                                     ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-
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02-MAR-2004 (TREWBLrel. 27, Created)
02-MAR-2004 (TREWBLrel. 27, Last sequence update)
02-MAR-2004 (TREWBLrel. 27, Last annotation update)
02-MAR-2004 (TREWBLrel. 27, Last annotation update)
Collal protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Mammary tumor;
Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J. Schmutz J., Myers R.M., Butterfield Y.S., Kzzywinski M.T., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 ---GFQGPPGEPGESGPGGSGPWGPRGPPGKNGDDGEAGKPGRPGERGFPGPARGLP
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al Similarity 56.0%; Pred. No. 1.5e-92;
510; Conservative 29; Mismatches 227; Indels 144;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

EMBL: BCOS2081, AAH55281.1 . .

EMBL: BCOS2081, AAH55281.1 . .

InterPro; IPR008161; Clalagen.

InterPro; IPR008161; Clalagen.

InterPro; IPR008161; Pibrinogen.C.

InterPro; IPR00885; Fibr.collagen.C.

InterPro; IPR00885; Fibr.collagen.C.

IR Ffam; PF00181; CCLF1; 1.

Pfam; PF00181; CCLF1; 1.

Probom; PD0020078; Fibr.collagen.C; 1.

Probom; PD0020078; Fibr.collagen.C; 1.

PROBOM; PR00038; VWC; 1.

PROSITE; PS01208; VWFC.1; 1.

PROSITE; PS01208; VWFC.1; 1.
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                                                                                                                                                                                                                                                                TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Mix FVB/N;
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                                                                                                                    73 PNPQRREGECCAFCPEEXVSPNSEDV-GVEGPKGDPGPQGPRGPVGPPGRDGIP
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                                                                           Gaps
                                                                           144;
                                          53.8%; Score 2494; DB 2; Length 1225; larity 56.0%; Pred. No. 1.5e-92; Conservative 29; Mismatches 227; Indels 144
EMBL; BC059281; AAH59281.1; -. SEQUENCE 1225 AA; 117860 MW; B6B86CBB4457F4D9 CRC64;
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